

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:37:01 ; Search time 30.701 Seconds
(without alignments)
2504.793 Million cell updates/sec

Title: US-09-811-131-32

Perfect score: 1547
Sequence: 1 MTDAAISPAKDFLAGVAAA.....LRGNGAFVLYVDEIKKKT 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriophage:*
17: SP_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1515	97.9	298	6	Q8GSH5
2	1450	93.7	298	11	Q8H10
3	1446	93.5	298	13	Q8PH1
4	1443	93.3	298	13	Q8PH2
5	1443	93.3	298	13	Q8PH3
6	1439	93.0	298	13	Q8PH4
7	1425	92.1	298	13	Q8PH5
8	1423	92.0	298	6	Q8GSH5
9	1417	91.6	298	11	Q8BVR7
10	1295	83.7	317	13	Q8I36
11	1278	82.6	299	5	Q8VX4
12	1253.5	81.0	312	5	Q8IRAO
13	1248.5	80.7	300	5	Q8HMS
14	1190.5	77.0	288	5	Q8A093
15	1185.5	76.6	288	5	Q8A094
16	1146	74.1	254	11	Q8BK5

17	1145.5	74.0	304	5	Q25129	Q25129 halocynthia
18	1125.5	72.8	307	5	Q62526	Q62526 drosophila
19	1102	71.2	315	4	Q9H0C2	Q9H0C2 homo sapien
20	1040.5	67.3	310	10	Q8H727	Q8H727 phytochlor
21	1032	66.7	300	5	Q45865	Q45865 caenorhabdi
22	1029	66.5	313	5	Q21103	Q21103 caenorhabdi
23	1029	66.5	313	5	P91410	P91410 caenorhabdi
24	986	63.7	300	5	Q01813	Q01813 caenorhabdi
25	985	63.7	309	5	Q97470	Q97470 dictyosteli
26	983	63.5	300	5	Q17407	Q17407 caenorhabdi
27	950.5	61.4	318	5	Q9BJ36	Q9BJ36 toxoplasma
28	949.5	61.4	307	8	Q9XM22	Q9XM22 ascaris suu
29	942	60.9	301	5	Q8I334	Q8I334 plasmodium
30	939	60.7	301	5	Q25692	Q25692 plasmodium
31	938	60.6	301	5	Q26006	Q26006 plasmodium
32	932	60.2	301	5	Q8MVR4	Q8MVR4 euploies sp
33	929	60.1	305	5	Q8MVR7	Q8MVR7 nyctotherus
34	925	59.8	308	5	Q8MVR8	Q8MVR8 nyctotherus
35	919	59.4	306	5	Q8MVR5	Q8MVR5 nyctotherus
36	915	59.1	308	5	Q8MVR6	Q8MVR6 nyctotherus
37	819	52.9	170	6	Q9X859	Q9X859 sus scrofa
38	778	50.3	305	3	Q9P8M1	Q9P8M1 yarrowia li
39	764.5	49.4	302	3	Q8J0M2	Q8J0M2 yarrowia li
40	759	49.1	326	5	P91270	P91270 caenorhabdi
41	755	48.8	303	3	Q74260	Q74260 candida par
42	753	48.7	317	5	Q9N647	Q9N647 leishmania
43	752	48.6	307	5	Q76286	Q76286 trypanosoma
44	750	48.5	386	10	P93767	P93767 lycopersico
45	749.5	48.4	306	5	Q18683	Q18683 caenorhabdi

ALIGNMENTS

RESULT 1

ID	Q8GSH5	PRELIMINARY	PRT:	298 AA.
AC	Q8GSH5			
DT	01-JUN-2002 (TREMBLrel. 21, Created)			
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Adenine nucleotide translocator 2.			
OS	Bos taurus (Bovine)			
OC	Karyofora; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Yamazaki N., Shinohara Y., Tanida K., Terada H.;			
RT	"Structural properties of mammalian mitochondrial ADP/ATP carriers:			
RT	Identification of possible amino acids that determine functional			
RT	differences in its isoforms."			
RL	Mitochondrion 1:371-379 (2002).			
DR	EMBL, AB065433; BAB84673.1;			
DR	InterPro; IPR001993; Mitochondrion carrier.			
DR	Pfam; PF00153; mito_catr; 3.			
DR	PROSITE; PS00215; MITOCH CARRIER; 3.			
SQ	SEQUENCE 298 AA; 32955 MW; CB6897BB987B79C0 CRC64;			

Query Match	97.9%	Score 1515;	DB 6;	Length 298;
Best Local Similarity	97.7%	Pred. No. 5.2e-126;		
Matches 291;	Conservative 4;	Mismatches 3;	Indels 0;	Gaps 0;
QY	1	MTDAAISPAKDFLAGVAAAISKRAVAPIERVKLLQVQHASKQITPDKOYKGIIDCVVR	60	
DB	1	MTDAAISPAKDFLAGVAAAISKRAVAPIERVKLLQVQHASKQITPDKOYKGIIDCVVR	60	
QY	61	IPKQEVLSFWRGVLANVIRFPPTQALNPAFKDKYKQIFLGVDKRTQFWRYFAGNLSG	120	
DB	61	IPKQGVLSFWRGVLANVIRFPPTQALNPAFKDKYKQIFLGVDKRTQFWRYFAGNLSG	120	
QY	121	GAAGTSLCPYPIPDPAFTLLADVGKAGAEERERGGDCLVTKYKSDGKGLYQGFNVS	180	

Db	121	GAAGATSLCVPYELDPARTLRADVKGAKAEPRFGDGLVKIKYKSDGINKGLVQGFNVLS	180
Qy	181	VQGIITYYRAAYFGIYDTAKGMLPDPKNTHIVISNMLAQTVRAVGLTSEYEDTYRRRRMM	240
Db	181	VQGIITYYRAAYFGIYDTAKGMLPDPKNTHIFISNMLAQTVRAVGLTSEYEDTYRRRRMM	240
Qy	241	QSGRKGTDIYATGTLDQCRKIARDEEGKAFPKGASNVLRGKGAFVVLVDLTKYKT	298
Db	241	QSGRKGTDIYATGTLDQCRKIARDEEGKAFPKGASNVLRGKGAFVVLVDLTKYKT	298

RESULT 2

AC 06A010; PRELIMINARY; PRT; 298 AA.
AD 06A010;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-Oct-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Solute carrier family 25 member 5 protein.
GN SLC25A5.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22035902; PubMed=12006978;
RA Golling G., Amsterdam A., Sun Z., Antonelli M., Maldonado E., Chen W.,
RA Burgess S., Haldi M., Artzt K., Farrington S., Lin S.-Y., Nissen R.M.,
RA Hopkins N.,
RT "Insertional mutagenesis in zebrafish rapidly identifies genes
RT essential for early vertebrate development."
RL Nat. Genet. 31:135-140(2002).
DR EMBL; AF506216; AAM34660.1; -.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mlt_carrier.
DR InterPro; IPR002030; Mlt_uncoupling.
DR Pfam; PF00153; mltc_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
QO SEQUENCE 298 AA; 32763 MW; D78663CF65C5D39 CR664;

	Query Marc3	Similarity	93.7%;	Score 1450;	DB 130;	Length 298;
	Best Local	Similarity	92.9%;	Prod. No. 36-120;		
	Matches	275;	Conservative	13;	Mismatches	8;
					Indels	0;
					Gaps	0
Qy	1	MTDAALSPANDPLAGVAAAIISTVAAPLERVKLLIQVQHASKQTADKQYKGIIDCYVR	60			
		::::				
Db	1	MSRTAISPADFDLAGGIIAAIISTVAAPLERVKLLIQVQHASKQTADKQYKGIIDCYVR	60			
Qy	61	IPREQELTSPWRGNLANVIRYFPTQALNPAFYDKYQIFLGVDKRTQFWRYPAGNLASG	120			
		::::				
Db	61	IPREQELTSPWRGNLANVIRYFPTQALNPAFYDKYQIFLGVDKRTQFWRYPAGNLASG	120			
Qy	121	GAAGATSLCYVYFLDPARTRLADVCKAAEEFPGFLDCLVKYIKSGIKGTYQSGNVS	180			
		::::				
Db	121	GAAGATSLCYVYFLDPARTRLADVCKAAEEFPGFLDCLVKYIKSGIKGTYQSGNVS	180			
Qy	181	VQGIITVRAAYFGCIYDTAKGMLPDPKNTHTIVISMMIAQTVTAVAGLTSPEDTVRRBMM	240			
		::::				
Db	181	VQGIITVRAAYFGCIYDTAKGMLPDPKNTHTIVISMMIAQTVTAVAGLTSPEDTVRRBMM	240			
Qy	241	QSGRKGVDTMYTGTLLDCWKRIADDEGKAPFGAASNTLRGCGAFVTVLYDELTCK	296			
		::::				
Db	241	QSGRKGVDTMYTGTLLDCWKRIADDEGKAPFGAASNTLRGCGAFVTVLYDELTCK	296			

RESULT 3

Q9PRH1	:	PRELIMINARY;	PRT;	298 AA
ID	Q9PRH1			

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AC Q9PRH1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (Wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_Taxid=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99083423; PubMed=9866197;
RA Miura I., Ohnishi H., Nakamura W., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
RT z, w, x, and y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, Adp/ATP translocase.";
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB008463; BA36513.1; -
DR EMBL; AB008456; BA36506.1; -
DR EMBL; AB008461; BA36511.1; -
DR EMBL; AB008462; BA36512.1; -
DR InterPro: IPR001993; Mitochond. carrier.
DR InterPro: IPR002067; Mit. carrier.
DR InterPro: IPR002030; Mit_coupling.
DR Pfam; PF00153; mito_cartr_3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA, 33054 MW, B0E23AD56F548D36 CRC64;

```

Query Match

Best local similarity 31.58; EREC.MO. 0.00 120;
Matches 273; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

QY	1	MTDALISAKPEIAGVAAAIISKTVA	PERVETKLLQVHASQITADQYKSI	IDCVVR	60
Db	1	MTDAIISAKPEIAGVAAAIISKTVA	PERVETKLLQVHASQITADQYKSI	IMCVVR	60
QY	61	IPKEQVLSFMRGNIANVIRYPTOLN	FAFOKTKQITLFGVDKETOQWRY	PAGNLSG	120
Db	61	IPKEQGFVSFMRGNIANVIRYPTOL	NFAFODKYKIKILDNVDKETOQW	RYPAGNLSG	120
QY	121	GAAGTSICFYVLELPARTRLAADY	GKGAERFPGIADCLVITYSDGI	KGLYQGFNV	180
Db	121	GAAGTSICFYVLELPARTRLAADY	GKGAERFPGIADCLVITYSDGI	KGLYQGFNV	180
QY	181	VGGIITYRAAYGIYDTAKGMLPDE	KRNTIIVISMMIAQTVTA	VAGLTSYSPEDTVRRMM	240
Db	181	VGGIITYRAAYGIYDTAKGMLPDE	KRNTIIVISMMIAQTVTA	VAGLTSYSPEDTVRRMM	240
QY	241	QSGRGCTIDMTGTCLDCKRIARDE	GKGRFPGANSNTVRMGGA	FVLVLYDEIKKY	297
Db	241	QSGRGGAISMTGCTIDCKRIARDE	GSRFPGANSNTVRMGGA	FVLVLYDEIKKY	297

RESULT 4

ID	Q9PRH2	PRELIMINARY;	FRT;	298 AA.
AC	Q9PRH2			
DT	01-MAY-2000 (TREMBLrel. 13)	Created		
DT	01-MAY-2000 (TREMBLrel. 13)	Last sequence update)		
DT	01-MAR-2003 (TREMBLrel. 23)	Last annotation update)		
DE	ADP/ATP translocase.			
OS	Rana rugosa (Winkled frog).			
CC	Euryarchaeota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana			
OX	NCBI_TaxID=8410;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99083429; PubMed=9866197;			
RA	Miyata I., Ohtani H., Nakamura M., Ichikawa Y., Satoh K.;			

RT "The origin and differentiation of the heteromorphic sex chromosomes
 RT Z, W, X, and Y in the frog *Rana rugosa*, inferred from the sequences of
 RT a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619(1998).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AB008460; BAA36510.1; -
 DR EMBL; AB008458; BAA36508.1; -
 DR EMBL; AB008459; BAA36509.1; -
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Membrane; Transmembrane; Transport.
 SQ SEQUENCE 298 AA; 33082 MW; BOB225E867599A06 CRC64;

Query Match 93.3%; Score 1443; DB 13; Length 298;
 Best Local Similarity 91.6%; Pred. No. 1.2e-119;
 Matches 272; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTDAAISPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKOITADKOYKGIIDCVNR 60
 DB 1 MTDAAISPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKOITADKOYKGIIDCVNR 60
 QY 61 IPKQEVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGGVDKRTQFMYRFGANLASG 120
 DB 61 IPKQEVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGGVDKRTQFMYRFGANLASG 120
 QY 61 IPKQGVFSPWRGNLANVIRYPTQALNPAFKDKYKQIFLGGVDKRTQFMYRFGANLASG 120
 DB 61 IPKQGVFSPWRGNLANVIRYPTQALNPAFKDKYKQIFLGGVDKRTQFMYRFGANLASG 120
 QY 121 GAAGATSLCFVYPLDFAFRTLLADVGKAGABERFGLGDCLVKIKSDGKIGLYQGFNV 180
 DB 121 GAAGATSLCFVYPLDFAFRTLLADVGKAGABERFGLGDCLVKIKSDGKIGLYQGFNV 180
 QY 121 VQGIIRAYRFGIYDTAKGMLPDPKNTHTIVISWMTAQVTAVALGTSYPTDTRRRMM 240
 DB 181 VQGIIRAYRFGIYDTAKGMLPDPKNTHTIVISWMTAQVTAVALGTSYPTDTRRRMM 240
 DB 181 VQGIIRAYRFGIYDTAKGMLPDPKNTHTIVISWMTAQVTAVALGTSYPTDTRRRMM 240
 QY 241 QSGRKGIDIMYTGTLDCMKRIADDEGKAFPKGAMSVNLGMGAFVLVLYDEIKKY 297
 DB 241 QSGRKGAIMYSGTIDCMKRIADDEGSRAPFKGAMSVNLGMGAFVLVLYDEIKKY 297

RESULT 5

Q8AYM3 PRELIMINARY; PRT; 298 AA.
 ID Q8AYM3
 AC Q8AYM3;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE ATP/ADP antiporter.
 GN AVANT.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Toyomizu M., Ueda M., Sato S., Seki Y., Sato K., Akiba Y.;
 RT "Cold-induced mitochondrial uncoupling and expression of chicken UCP
 RT and ANT mRNA in chicken skeletal muscle.";
 RL FEBS Lett. 0:0-0(2002).
 DR EMBL; AB088686; BAC15533.1; -
 SQ SEQUENCE 298 AA; 32847 MW; 1174CC5EC400A10D CRC64;

Query Match 93.3%; Score 1443; DB 13; Length 298;
 Best Local Similarity 92.9%; Pred. No. 1.2e-119;
 Matches 275; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 MTDAAISPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKOITADKOYKGIIDCVNR 60
 DB 1 MTDAAISPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKOITADKOYKGIIDCVNR 60

QY 61 IPKQEVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGGVDKRTQFMYRFGANLASG 120
 DB 61 IPKQGVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGGVDKRTQFMYRFGANLASG 120
 QY 121 GAAGATSLCFVYPLDFAFRTLLADVGKAGABERFGLGDCLVKIKSDGKIGLYQGFNV 180
 DB 121 GAAGATSLCFVYPLDFAFRTLLADVGKAGABERFGLGDCLVKIKSDGKIGLYQGFNV 180
 QY 121 VQGIIRAYRFGIYDTAKGMLPDPKNTHTIVISWMTAQVTAVALGTSYPTDTRRRMM 240
 DB 181 VQGIIRAYRFGIYDTAKGMLPDPKNTHTIVISWMTAQVTAVALGTSYPTDTRRRMM 240
 QY 181 VQGIIRAYRFGIYDTAKGMLPDPKNTHTIVISWMTAQVTAVALGTSYPTDTRRRMM 240
 DB 181 VQGIIRAYRFGIYDTAKGMLPDPKNTHTIVISWMTAQVTAVALGTSYPTDTRRRMM 240
 QY 241 QSGRKGIDIMYTGTLDCMKRIADDEGKAFPKGAMSVNLGMGAFVLVLYDEIKKY 296
 DB 241 QSGRKGADIMYSGTIDCMKRIADDEGKAFPKGAMSVNLGMGAFVLVLYDEIKKY 296

RESULT 6

Q9YTC4 PRELIMINARY; PRT; 298 AA.
 ID Q9YTC4
 AC Q9YTC4;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE ADP/ATP translocase.
 OS *Rana rugosa* (Wrinkled frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OC NCBI_TaxID=8410;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=9083429; PubMed=9866197;
 RA Mura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
 RT "The origin and differentiation of the heteromorphic sex chromosomes
 RT Z, W, X, and Y in the frog *Rana rugosa*, inferred from the sequences of
 RT a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619(1998).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AB008457; BAA36507.1; -
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Membrane; Transmembrane; Transport.
 SQ SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00 CRC64;

Query Match 93.0%; Score 1439; DB 13; Length 298;
 Best Local Similarity 91.2%; Pred. No. 2.8e-119;
 Matches 271; Conservative 16; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTDAAISPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKOITADKOYKGIIDCVNR 60
 DB 1 MTDAAISPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKOITADKOYKGIIDCVNR 60
 QY 61 IPKQEVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGGVDKRTQFMYRFGANLASG 120
 DB 61 IPKQGVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGGVDKRTQFMYRFGANLASG 120
 QY 61 IPKQGVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGGVDKRTQFMYRFGANLASG 120
 DB 61 IPKQGVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGGVDKRTQFMYRFGANLASG 120
 QY 121 GAAGATSLCFVYPLDFAFRTLLADVGKAGABERFGLGDCLVKIKSDGKIGLYQGFNV 180
 DB 121 GAAGATSLCFVYPLDFAFRTLLADVGKAGABERFGLGDCLVKIKSDGKIGLYQGFNV 180
 QY 121 VQGIIRAYRFGIYDTAKGMLPDPKNTHTIVISWMTAQVTAVALGTSYPTDTRRRMM 240
 DB 181 VQGIIRAYRFGIYDTAKGMLPDPKNTHTIVISWMTAQVTAVALGTSYPTDTRRRMM 240
 DB 181 VQGIIRAYRFGIYDTAKGMLPDPKNTHTIVISWMTAQVTAVALGTSYPTDTRRRMM 240
 QY 241 QSGRKGIDIMYTGTLDCMKRIADDEGKAFPKGAMSVNLGMGAFVLVLYDEIKKY 297
 DB 241 QSGRKGAIMYSGTIDCMKRIADDEGSRAPFKGAMSVNLGMGAFVLVLYDEIKKY 297

RESULT 7

0919M9 PRELIMINARY; PRT; 298 AA.
 ID 0919M9
 AC 0919M9
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Adenine nucleotide translocase.
 GN AATL.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 CC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Crawford M.J., Kiosrowskian F., Varmuza S.L., Liverage R.A.;
 RT "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific and
 RT Dynamic Patterns of Expression During Development."
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL, AF21347; AAF6471.1; -.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mlt_carrier.
 DR InterPro; IPR002030; Mlt_uncoupling.
 DR Pfam; PF00153; mlt_carri_3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 DR Membrane; Transmembrane; Transport.
 SQ SEQUENCE 298 AA; 32940 MW; 91B740133751877F CRC64;

Query Match 92.1%; Score 1425; DB 13; Length 298;
 Best Local Similarity 91.6%; Pred. No. 4,9e-118;
 Matches 271; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADKQYKGIIDCVR 60
 DB 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADKQYKGIIDCVR 60
 QY 61 IPKEQEVLSFWRGKLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
 DB 61 IPKEQEVLSFWRGKLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
 QY 121 GAAGTSLCFYVPLDPFATRLAADVGKAGAREPGLDCLVIKYSKGIKGLYOGFNVS 180
 DB 121 GAAGTSLCFYVPLDPFATRLAADVGKAGAREPGLDCLVIKYSKGIKGLYOGFNVS 180
 QY 181 VGGIITVAAAFGYIDTAKGMLPDPKNTHTIVSNMIAQTVTAVALGTSYPTVRRMM 240
 DB 181 VGGIITVAAAFGYIDTAKGMLPDPKNTHTIVSNMIAQTVTAVALGTSYPTVRRMM 240
 QY 241 VGGIITVAAAFGYIDTAKGMLPDPKNTHTIVSNMIAQTVTAVALGTSYPTVRRMM 240
 DB 241 VGGIITVAAAFGYIDTAKGMLPDPKNTHTIVSNMIAQTVTAVALGTSYPTVRRMM 240
 QY 241 QSGRKGADIMVTGTLDCWKRIARDEGKAFKFGKANSNVLKMGAFVLYVDEIKY 296
 DB 241 QSGRKGADIMVTGTLDCWKRIARDEGKAFKFGKANSNVLKMGAFVLYVDEIKY 296

RESULT 8

046373 PRELIMINARY; PRT; 298 AA.
 ID 046373
 AC 046373
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE ADP/ATP translocase.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 CC NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Skeletal muscle;
 RA Yamaguchi N., Kasai M.;
 RT "Identification of a 30kDa calsequestrin-binding protein, which
 RT regulates calcium release from sarcoplasmic reticulum of rabbit
 RT skeletal muscle."
 RL J. Biochem. 335:541-547(1998).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL, AB009386; BAA23777.1; -.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mlt_carrier.
 DR InterPro; IPR002030; Mlt_uncoupling.
 DR Pfam; PF00153; mlt_carri_3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 DR Membrane; Transmembrane; Transport.
 SQ SEQUENCE 298 AA; 32901 MW; CABA32C88164AD78 CRC64;

Query Match 92.0%; Score 1423; DB 6; Length 298;
 Best Local Similarity 89.9%; Pred. No. 7,4e-118;
 Matches 267; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADKQYKGIIDCVR 60
 DB 1 MSDQSLFLKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKQISAKQYKGIIDCVR 60
 QY 61 IPKEQEVLSFWRGKLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
 DB 61 IPKEQEVLSFWRGKLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
 QY 121 GAAGTSLCFYVPLDPFATRLAADVGKAGAREPGLDCLVIKYSKGIKGLYOGFNVS 180
 DB 121 GAAGTSLCFYVPLDPFATRLAADVGKAGAREPGLDCLVIKYSKGIKGLYOGFNVS 180
 QY 181 VGGIITVAAAFGYIDTAKGMLPDPKNTHTIVSNMIAQTVTAVALGTSYPTVRRMM 240
 DB 181 VGGIITVAAAFGYIDTAKGMLPDPKNTHTIVSNMIAQTVTAVALGTSYPTVRRMM 240
 QY 241 QSGRKGADIMVTGTLDCWKRIARDEGKAFKFGKANSNVLKMGAFVLYVDEIKY 297
 DB 241 QSGRKGADIMVTGTLDCWKRIARDEGKAFKFGKANSNVLKMGAFVLYVDEIKY 297

RESULT 9

088V19 PRELIMINARY; PRT; 298 AA.
 ID 088V19
 AC 088V19
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Solute carrier family 25.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL; AK078077; BAC37117.1; -.
 SQ SEQUENCE 298 AA; 32904 MW; F94C8909836710B CRC64;

Query Match 91.6%; Score 1417; DB 11; Length 298;
 Best Local Similarity 89.6%; Pred. No. 2,5e-117;
 Matches 266; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADKQYKGIIDCVR 60
 DB 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADKQYKGIIDCVR 60

Db 1 MGDKALSPKDFLAGGAAVAVKTAVERVLLQVQHASKOJSAEKQYGIIDCVR 60
 QY 61 IPKEQVLSFMRGNLANVIRYPTQALNFAFDKXKQIFLGVDVDRTOFMRFAFNLASG 120
 Db 61 IPKEQGFISFMRGNLANVIRYPTQALNFAFDKXKQIFLGVDVDRTOFMRFAFNLASG 120
 QY 121 GAAGATSLCFVYPLDPFARTRLAADVGKAGAREFRGLDCLVKIYKSDIGKLYOGFNV 180
 Db 121 GAAGATSLCFVYPLDPFARTRLAADVGKAGAREFRGLDCLVKIYKSDIGKLYOGFNV 180
 QY 181 VGGIIIRYAAVFGYDIAKGMPLDPKNTPIVISMIAQTVTAAGLTSYPTVARRMM 240
 Db 181 VGGIIIRYAAVFGYDIAKGMPLDPKNTPIVISMIAQSVTAAGLTSYPTVARRMM 240
 QY 241 OSGRKGTIMYTGTLDCWKRKLARDGKGAFFKGAASNTLRGGAFLVLYDEIKKY 297
 Db 241 OSGRKGTIMYTGTLDCWKRKLARDGKGAFFKGAASNTLRGGAFLVLYDEIKKY 297

RESULT 10
 ID 091336 PRELIMINARY; PRT; 317 AA.
 AC 091336;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-MAR-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE ADP/ATP translocase
 OS Rana sylvatica (Wood frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
 NCBI_TaxID=45438;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=97398141; PubMed=9256066;
 RA Cai Q., Greenway S.C., Storey K.B.;
 RT "Differential regulation of the mitochondrial ADP/ATP translocase gene
 in wood frogs under freezing stress";
 RL Biochim. Biophys. Acta 1353:69-78(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Cai Q., Storey K.B.;
 RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; U44932; AAA97882.2; -
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR Pfam; PF00153; mito_carrier_3.
 DR PRINTS; PS00926; MITOCH_CARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KM Membrane; Transmembrane; Transport.
 SQ SEQUENCE 317 AA; 35005 MW; 5F6B7EDBD5CEB72 CRC64;

Query Match 83.7%; Score 1295; DB 13; Length 317;
 Best Local Similarity 90.1%; Pred. No. 1.7e-106;
 Matches 245; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTDAAISPAKDFLAGGAAVAVKTAVERVLLQVQHASKOJTDADQYGIIDCVR 60
 Db 1 MTDAAISPAKDFLAGGAAVAVKTAVERVLLQVQHASKOJTDADQYGIIDCVR 60
 QY 61 IPKEQVLSFMRGNLANVIRYPTQALNFAFDKXKQIFLGVDVDRTOFMRFAFNLASG 120
 Db 61 IPKEQGFISFMRGNLANVIRYPTQALNFAFDKXKQIFLGVDVDRTOFMRFAFNLASG 120
 QY 121 GAAGATSLCFVYPLDPFARTRLAADVGKAGAREFRGLDCLVKIYKSDIGKLYOGFNV 180
 Db 121 GAAGATSLCFVYPLDPFARTRLAADVGKAGAREFRGLDCLVKIYKSDIGKLYOGFNV 180
 QY 181 VGGIIIRYAAVFGYDIAKGMPLDPKNTPIVISMIAQTVTAAGLTSYPTVARRMM 240
 Db 181 VGGIIIRYAAVFGYDIAKGMPLDPKNTPIVISMIAQSVTAAGLTSYPTVARRMM 240

QY 241 OSGRKGTIMYTGTLDCWKRKLARDGKGAFFKGAASNTLRGGAFLVLYDEIKKY 297
 Db 241 OSGRKGTIMYTGTLDCWKRKLARDGKGAFFKGAASNTLRGGAFLVLYDEIKKY 297

RESULT 11
 ID 095VX4 PRELIMINARY; PRT; 299 AA.
 AC 095VX4;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE ADP-ATP translocator.
 OS Ethmostigmus rubripes.
 OC Eukaryota; Metazoa; Arthropoda; Myriapoda; Chilopoda;
 OC Pleurostigmophora; Scolopendromorpha; Scolopendridae; Ethmostigmus.
 NCBI_TaxID=62613;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Burnell J.N.;
 RT "Nucleotide sequence of an ADP-ATP translocator of Ethmostigmus
 rubripes";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF401758; AAL02100.1; -
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR Pfam; PF00153; mito_carrier_3.
 DR PRINTS; PS00926; MITOCH_CARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 SQ SEQUENCE 299 AA; 33037 MW; 3C3B8CB267C3C58 CRC64;

Query Match 82.6%; Score 1278; DB 5; Length 299;
 Best Local Similarity 82.8%; Pred. No. 5.2e-105;
 Matches 241; Conservative 22; Mismatches 28; Indels 0; Gaps 0;

QY 5 AASPAKDFLAGGAAVAVKTAVERVLLQVQHASKOJTDADQYGIIDCVR 64
 Db 5 AASPAKDFLAGGAAVAVKTAVERVLLQVQHASKOJTDADQYGIIDCVR 64
 QY 65 QEVLSFMRGNLANVIRYPTQALNFAFDKXKQIFLGVDVDRTOFMRFAFNLASG 124
 Db 65 QEVLSFMRGNLANVIRYPTQALNFAFDKXKQIFLGVDVDRTOFMRFAFNLASG 124
 QY 125 ATSLCFVYPLDPFARTRLAADVGKAGAREFRGLDCLVKIYKSDIGKLYOGFNV 184
 Db 125 ATSLCFVYPLDPFARTRLAADVGKAGAREFRGLDCLVKIYKSDIGKLYOGFNV 184
 QY 185 IYRAAAYFGYDIAKGMPLDPKNTPIVISMIAQTVTAAGLTSYPTVARRMM 244
 Db 185 IYRAAAYFGYDIAKGMPLDPKNTPIVISMIAQTVTAAGLTSYPTVARRMM 244
 QY 245 KGTIDIMYTGTLDCWKRKLARDGKGAFFKGAASNTLRGGAFLVLYDEIK 295
 Db 245 KGTIDIMYTGTLDCWKRKLARDGKGAFFKGAASNTLRGGAFLVLYDEIK 295

RESULT 12
 ID 081RA0 PRELIMINARY; PRT; 312 AA.
 AC 081RA0;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE CG16944-PC.
 GN SE8B.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peerygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.

RA MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amaratunga P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abill J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brotter A.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Doudon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glaeser K.,
 RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman J.D., Hernandez J.R., Houck J.,
 RA Hostein D., Houston K.A., Howland T.J., Wei M.H., Idegawa C.,
 RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
 RA Laeso P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Melnikov G., Milshina N.V., Modarres C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kimnos I., Simpson M., Skupski M.P., Smith T.,
 RA Spletter B., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of Drosophila melanogaster";
 RA Science 287:2185-2195 (2000).
 [2]
 RP SEQUENCE FROM N.A.
 RA Celniker S.E., Adams M.D., Krommiller B., Man K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amaratunga P.G., Brandon R.C., Rogers Y.,
 RA Bantz J., An H., Baldwin D., Bantz J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorett V., Doup L.E., Doyle C., Dreene D., Farfan D.,
 RA Ferriera S., Frise E., Galle R.F., Gary N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwan C., Jaitai M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacle J.M., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RA "Sequencing of Drosophila melanogaster genome";
 RA Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A.
 RA Miara S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
 RA Clump M., Drysdale R., Emmert D., Frise B., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RA "Annotation of Drosophila melanogaster genome";
 RA Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter J.C.;
 RA Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 [5]
 RP SEQUENCE FROM N.A.

RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/Genbank/DBJ databases.
 RA EMBL; AE003484; AAN09267.1;
 SQ SEQUENCE 312 AA; 34214 MW; 78D5834E74E168DF CRC64;
 Query Match 81.0%; Score 1253.5; DB 5; Length 312;
 Best Local Similarity 81.2%; Pred. No. 8.1e-103;
 Matches 237; Conservative 21; Mismatches 33; Indels 1; Gaps 1;
 QY 5 A L S F A K D L A G V A A A I S K T A V A P E R V K L L Q V H A S K Q I T A D K Q Y G I I D C V R I P K E 64
 DB 20 A V G F Y K D P A A G I S A A V K T A V A P E R V K L L Q V H I S K Q I S P D K Q Y G M D C F R I P K E 79
 QY 65 Q E V L S F W R G N T A N V I R Y P P T Q A L N F A F D K Y K Q I F L G V D K R T Q F W R Y P A G N L A S G A A G 124
 DB 80 Q G F S F W R G N T A N V I R Y P P T Q A L N F A F D K Y K Q V F L G V D K R T Q F W R Y P A G N L A S G A A G 139
 QY 125 A T S I C F V Y P L D P A R T R L A A D V G K A E E P R F G D D C V K I Y K S D I K G L Y O G F N V S Y O G I 184
 DB 140 A T S I C F V Y P L D P A R T R L A A D V G K - G G Q R E F T G L G N C L T Y K R S D E I V G L Y K G F V S Y O G I 198
 QY 185 I I Y R A A Y F G I Y D T A K G M L P D E K N T H I V S M M I A Q T V T A V A G L T S Y P F D T V R R M M Q S G R 244
 DB 199 I I Y R A A Y F G I D T A R G M L P D K N T P I Y S M A I A Q V T T V A G I V S Y P F D T V R R M M Q S G R 258
 QY 245 K G T D I M Y T G T I D C W R K I A R D E G K A F F K G A N S V I R G M G A F V L Y D E I K X 296
 DB 259 K A T E V I Y N T L H C W A T I A K Q R G T G A F F K G A F S N I L R G T G A F V L Y D E I K X 310
 RESULT 13
 ID Q9NHWS PRELIMINARY; PRT; 300 AA.
 GNHWS
 AC Q9NHWS; 1-103 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMblrel. 23, Last annotation update)
 DE ADP/ATP translocase.
 OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Lucilia.
 OX NCBI_TaxID=7375;
 [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=SS mal seeking;
 RA Chen Z., Fair J.A., Batterham P.;
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC EMBL; AF218587; AAF2322.1;
 DR EMBL; AF218587; AAF2322.1;
 DR InterPro; IPR001993; Mitoch carrier.
 DR InterPro; IPR002067; Mit carrier.
 DR Pfam; PF00153; mltc_carr_3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER, 3.
 KW Membrane; Transmembrane; Transport.
 SQ SEQUENCE 300 AA; 33036 MW; 5459DF0EA0E2E742 CRC64;
 Query Match 80.7%; Score 1248.5; DB 5; Length 300;
 Best Local Similarity 81.2%; Pred. No. 2.1e-102;
 Matches 237; Conservative 20; Mismatches 34; Indels 1; Gaps 1;
 QY 6 L S F A K D L A G V A A A I S K T A V A P E R V K L L Q V H A S K Q I T A D K Q Y G I I D C V R I P K E 65
 DB 9 L G F Y K D P A A G I S A A V K T A V A P E R V K L L Q V H I S K Q I S P D K Q Y G M D C F R I P K E 68
 QY 66 E V L S F W R G N T A N V I R Y P P T Q A L N F A F D K Y K Q I F L G V D K R T Q F W R Y P A G N L A S G A A G 125
 DB 69 G F A S Y F W R G N T A N V I R Y P P T Q A L N F A F D K Y K Q V F L G V D K R T Q F W R Y P A G N L A S G A A G 128
 QY 126 T S L C F V Y P L D P A R T R L A A D V G K A E E P R F G D D C V K I Y K S D I K G L Y O G F N V S Y O G I 185

Db 129 TSLCFVYPLDPAFRTLAADTGK-GGQREFTGLNGCLAKIFKSDGLVGLRGFVSGI 187
 Qy 186 IYRAAYFPIYDTAKMPLDPKNTHTVISMMLAQVTAAAGLTSYFPDVRMMMOGRK 245
 Db 188 IYRAAYFPIYDTAKMPLDPKNTHTVISMMLAQVTAAAGLTSYFPDVRMMMOGRK 247
 Qy 246 GTDITMTGTLDCWKRIARDEGKAFPKGAMSNVLRGMAFVLYYDEIKK 297
 Db 248 ATETIYKNTLHCWATIAKQEGAFKGAFSNVLKGTGAFVLYYDEIKK 299

RESULT 14

O44093 PRELIMINARY: PRT: 288 AA.

Id 044093
 AC 044093
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE ADP/ATP translocase (Fragment).
 GN SESH.
 OS Drosophila pseudobscura (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7237;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zeng L.-W., Comeran J.M., Chen B., Kreitman M.;
 RL Genetics 0:0-0(1997).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF025799; AAB87884.1; -.
 DR FlyBase: FBgn0023237; Dmub\seeb.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR Pfam: PF00153; mltc_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Membrane; Repeat; Transmembrane; Transport.
 FT NON_TER 288
 SQ SEQUENCE 288 AA; 31725 MW; 052B0CC0050436B0 CRC64;

Query Match 77.0%; Score 1190.5; DB 5; Length 288;
 Best Local Similarity 80.4%; Pred. No. 2.8e-97;
 Matches 229; Conservative 20; Mismatches 33; Indels 3; Gaps 3;

Qy 5 ALSFAKDPLAGVAAAIKTAAPIERVYKLLQVQHSKQITADKQYGIIDCVIRIPKE 64
 Db 7 AIGFVKDPAAGGISAASVKTAVAPIERVYKLLQVQHSKQISPDQYKGMVDCFRIPKE 66
 Qy 65 QEVLSFMRGNLANVIRYPTQALNFAFDKTKQIFLGVDKRTQFWRFPAGNLASGGAG 124
 Db 67 QGFSSFMWGNLANVIRYPTQALNFAFDKTKQIFLGVDKRTQFWRFPAGNLASGGAG 126
 Qy 125 ATSLCFVYPLDPAFRTLAADVAGKAGREBFRGLADCLVKIYKSDGIKGLYOGFNVSVOGI 184
 Db 127 ATSLCFVYPLDPAFRTLAADTGK-GGQREFTGLNGCLTKIFKSDGLVGLRGFVSGI 185
 Qy 185 IYRAAYFGIYDTAKMPLDPKNTHTVISMMLAQVTAAAGLTSYFPDVRMMMOGR 244
 Db 186 IYRAAYFGIYDTAKMPLDPKNTHTVISMMLAQVTAAAGLTSYFPDVRMMMOGR 244
 Qy 245 KGTDMTGTLDCKWKRIARDEGKAFPKGAMSNVLRGMAFVLYY 289
 Db 245 KATEIYKNTLHCWATIAKQEGAFKGAFSNVLKGTGAFVLYY 288

RESULT 15

O44094 PRELIMINARY: PRT: 288 AA.

Id 044094
 AC 044094
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE ADP/ATP translocase (Fragment).

GN SESH.
 OS Drosophila subobscura (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7241;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zeng L.-W., Comeran J.M., Chen B., Kreitman M.;
 RL Genetics 0:0-0(1997).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF025799; AAB87884.1; -.
 DR FlyBase: FBgn0023237; Dmub\seeb.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR Pfam: PF00153; mltc_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Membrane; Repeat; Transmembrane; Transport.
 FT NON_TER 288
 SQ SEQUENCE 288 AA; 31775 MW; 06A1D1E477B81B26 CRC64;

Query Match 76.6%; Score 1185.5; DB 5; Length 288;
 Best Local Similarity 80.0%; Pred. No. 7.7e-97;
 Matches 228; Conservative 21; Mismatches 33; Indels 3; Gaps 3;

Qy 5 ALSFAKDPLAGVAAAIKTAAPIERVYKLLQVQHSKQITADKQYGIIDCVIRIPKE 64
 Db 7 AMGFVKDPAAGGISAASVKTAVAPIERVYKLLQVQHSKQISPDQYKGMVDCFRIPKE 66
 Qy 65 QEVLSFMRGNLANVIRYPTQALNFAFDKTKQIFLGVDKRTQFWRFPAGNLASGGAG 124
 Db 67 QGFSSFMWGNLANVIRYPTQALNFAFDKTKQIFLGVDKRTQFWRFPAGNLASGGAG 126
 Qy 125 ATSLCFVYPLDPAFRTLAADVAGKAGREBFRGLADCLVKIYKSDGIKGLYOGFNVSVOGI 184
 Db 127 ATSLCFVYPLDPAFRTLAADTGK-GGQREFTGLNGCLTKIFKSDGLVGLRGFVSGI 185
 Qy 185 IYRAAYFGIYDTAKMPLDPKNTHTVISMMLAQVTAAAGLTSYFPDVRMMMOGR 244
 Db 186 IYRAAYFGIYDTAKMPLDPKNTHTVISMMLAQVTAAAGLTSYFPDVRMMMOGR 244
 Qy 245 KGTDMTGTLDCKWKRIARDEGKAFPKGAMSNVLRGMAFVLYY 289
 Db 245 KATEIYKNTLHCWATIAKQEGAFKGAFSNVLKGTGAFVLYY 288

Search completed: December 18, 2003, 12:43:10
 Job time : 31.701 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:36:16 / Search time 8.34267 Seconds
(without alignments)
1679.794 Million cell updates/sec

Title: US-09-811-131-33

Perfect score: 1543

Sequence: 1 MTEQALSPAKFLAGTAA.....LRGNGAFVLYVDELKVTI 298

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1543	100.0	298	ADT3_HUMAN	P12236 homo sapien
2	1512	98.0	298	ADT3_BOVIN	P32007 boe tauru
3	1463	94.8	298	ADT2_HUMAN	P05141 homo sapien
4	1451	94.0	298	ADT2_RAT	Q09073 rattus norv
5	1445	93.6	298	ADT2_MOUSE	P51881 mus musculu
6	1424	92.3	298	ADT1_RAT	Q05962 rattus norv
7	1418	91.9	298	ADT1_MOUSE	P48962 mus musculu
8	1417	91.8	297	ADT1_BOVIN	P02722 boe tauru
9	1409	91.3	298	ADT1_HUMAN	P12235 homo sapien
10	1254.5	81.3	299	ADT_EKOME	Q26365 drosophila
11	1204	78.0	301	ADT_ANOGA	Q27238 anopheles g
12	978	63.4	339	ADT_CHLKE	P31692 chlorella k
13	778.5	50.5	307	ADT3_YEAST	P18238 saccharomyc
14	772	50.0	308	ADT_CHLKE	P27080 chlamydomon
15	769	49.8	322	ADT_SCHPO	Q09188 schizosacch
16	768	49.8	386	ADT1_GOSHI	Q22342 gossypium h
17	766	49.6	313	ADT_NEUCR	P02723 neurospora
18	762.5	49.4	305	ADT_KULIA	P48382 kluyveromyc
19	760.5	49.3	318	ADT2_YEAST	P18239 saccharomyc
20	750	48.6	385	ADT2_ARATH	P44929 arabidopsis
21	750	48.6	387	ADT1_MAIZE	P04709 zea mays (m
22	748	48.5	386	ADT1_SOLTU	P25083 solanum tub
23	747	48.4	382	ADT_OKISA	P18571 oryza sativ
24	744	48.2	387	ADT2_MAIZE	P18571 zea mays (m
25	742.5	48.0	381	ADT1_ARATH	P31167 arabidopsis
26	740	47.9	331	ADT1_ARATH	P41629 triticum ae
27	739.5	47.9	386	ADT2_SOLTU	P27081 solanum tub
28	737.5	47.8	309	ADT1_YEAST	P04710 saccharomyc
29	727	47.1	331	ADT2_WHEAT	Q41630 triticum ae
30	305.5	19.8	565	CMC3_CABEL	Q19529 caenorhabdi
31	302	19.6	588	CMC2_CABEL	Q20799 caenorhabdi
32	300	19.4	330	GDC_BOVIN	Q01888 boe tauru
33	299	19.4	307	ODC2_YEAST	Q99297 saccharomyc

34	295	19.1	678	1	CMC1_HUMAN	O75746 homo sapien
35	289.5	18.8	322	1	GDC_RAT	P16261 rattus norv
36	287.5	18.6	702	1	CMC1_CABEL	O21153 caenorhabdi
37	286	18.5	325	1	UCP5_HUMAN	O95258 homo sapien
38	285	18.5	332	1	GDC_HUMAN	P16260 homo sapien
39	284	18.4	325	1	UCP5_MOUSE	Q922b2 mus musculu
40	282.5	18.3	326	1	YCB8_SCHPO	O13805 schizosacch
41	280	18.1	675	1	CMC2_HUMAN	O9160 homo sapien
42	272	17.6	315	1	MPT_HUMAN	O912d1 homo sapien
43	270	17.5	315	1	SH18_HUMAN	O91k4 homo sapien
44	265	17.2	312	1	UCP3_HUMAN	P55916 homo sapien
45	265	17.2	676	1	CMC2_MOUSE	Q9gxx4 mus musculu

ALIGNMENTS

RESULT 1
ADT3_HUMAN STANDARD; PRT; 298 AA.
AC P12236; Q96C49;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADP/ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3)
DE (Adenine nucleotide translocator 3) (ANT 3).
GN SLC25A6 OR ANT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Metazoa; Primates; Carnivora; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89236396; PubMed=2541251;
RA Cozens A.L., Runswick M.J., Walker J.E.;
RT "DNA sequences of two expressed nuclear genes for human mitochondrial
ADP/ATP translocase.";
RL J. Mol. Biol. 206:261-280(1989).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,
Margolin J.F.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, Cervix, Eye, and Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klauser R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Dietzenko L., Marzella K., Farmer A.A., Rubin G.M., Hong L.,
Stromberg M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Guarnate P.H.,
Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Faley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzyzinski M.I., Skalek U., Smalhus D.E.,
Schnerlich J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 36-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houldsworth J., Attardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA

RT level in adult human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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 CC -----
 CC EMBL, J03592; AAA36750.1; -;
 DR EMBL, AY007135; AAG01998.1; -;
 DR EMBL, BC007295; AAH07295.1; -;
 DR EMBL, BC007850; AAH07850.1; -;
 DR EMBL, BC008737; AAH08737.1; -;
 DR EMBL, BC008935; AAH08935.1; -;
 DR EMBL, BC014775; AAH14775.1; -;
 DR EMBL, S03894; S03894.
 DR GeneW; HGNC:10992; SLC25A6.
 DR MIM; 300151; -;
 DR GO; GO:0005744; C:mitochondrial inner membrane translocase co. .; TMS.
 DR GO; GO:0005471; P:ATP/ADP antiporter activity; NAS.
 DR GO; GO:0006854; P:ATP/ADP exchange; TMS.
 DR InterPro; IPR002067; Mlt carrier.
 DR InterPro; IPR002030; Mlt uncoupling.
 DR Pfam; PF00153; mltc_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 100 1.
 FT REPEAT 101 208 2.
 FT REPEAT 209 298 3.
 FT REPEAT 209 298 3.
 FT CONFLICT 105 108 KTO -> RHA (IN REF. 4).
 FT CONFLICT 242 242 S -> F (IN REF. 3; AAH14775).
 SQ SEQUENCE 298 AA; 32866 MW; 1853489F0849672F CRC64;
 Query Match 100.0%; Score 1543; DB 1; Length 298;
 Best Local Similarity 100.0%; Pred. No. 3.6e-128;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 MTEQAISPAKDFLAGIAAIAISKTAAPIERVKLLQVOHASKOIAADKOYGIYDCLVR 60
 Db 1 MTEQAISPAKDFLAGIAAIAISKTAAPIERVKLLQVOHASKOIAADKOYGIYDCLVR 60
 Oy 1 IPRKQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVCKHTQFWRYFAGNLASG 120
 Db 1 IPRKQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVCKHTQFWRYFAGNLASG 120
 Oy 61 IPRKQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVCKHTQFWRYFAGNLASG 120
 Db 61 IPRKQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVCKHTQFWRYFAGNLASG 120
 Oy 121 GAAGTSTLCFYPPDPAFTRILAADVKGSTEREFGDCLVYTKSGIKGLYGSFVS 180
 Db 121 GAAGTSTLCFYPPDPAFTRILAADVKGSTEREFGDCLVYTKSGIKGLYGSFVS 180
 Oy 181 VGGIITTAAYFAGVDTAKGMLPDKKNTHTIVVSMIAQTAVAVAGVSPPTVARRMM 240
 Db 181 VGGIITTAAYFAGVDTAKGMLPDKKNTHTIVVSMIAQTAVAVAGVSPPTVARRMM 240

Oy 241 QSGRRKADIMTYGVDCWRKIFRDEGKAFKAGANSVLRMGAFVLVYDELKKVI 298
 Db 241 QSGRRKADIMTYGVDCWRKIFRDEGKAFKAGANSVLRMGAFVLVYDELKKVI 298
 RESULT 2
 ID ADT3 BOVIN STANDARD; PRT; 298 AA.
 AC P32007;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP/ATP carrier protein, isoform T2 (ADP/ATP translocase 3) (Adenine
 DE nucleotide translocator 3) (ANT 3).
 OS SLC25A6 OR ANT3.
 OS Bos taurus (Bovine).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89223093; PubMed=2540808;
 RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
 RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
 RT differences in various tissues."
 RL Biochemistry 28:866-873(1989).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, M24103; AAA30769.1; -;
 DR PIR; B43646; B43646.
 DR InterPro; IPR002067; Mlt carrier.
 DR InterPro; IPR002030; Mlt uncoupling.
 DR InterPro; IPR001993; Mltc_carr; 3.
 DR Pfam; PF00153; mltc_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 100 1.
 FT REPEAT 101 208 2.
 FT REPEAT 209 298 3.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32877 MW; 1C34E7DE6E54061 CRC64;
 Query Match 98.0%; Score 1512; DB 1; Length 298;
 Best Local Similarity 97.7%; Pred. No. 1.9e-125;
 Matches 291; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 MTEQAISPAKDFLAGIAAIAISKTAAPIERVKLLQVOHASKOIAADKOYGIYDCLVR 60
 Db 1 MTEQAISPAKDFLAGIAAIAISKTAAPIERVKLLQVOHASKOIAADKOYGIYDCLVR 60

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QY 61 IPKEQVLSFWKGNLANVIRPPTOALNPAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120
DB 61 IPKEQVLSFWKGNLANVIRPPTOALNPAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDPARTRLADVKGSGTEREFGDCLVKTYSKGIRGLYOGFSVS 180
DB 121 GAAGATSLCFVYPLDPARTRLADVKGSGTEREFGDCLVKTYSKGIRGLYOGFSVS 180
QY 181 VGGIITRYAAVFGYVDTAKGMLPDPKXNTHIVVSMIAQTVAAGVVSYPEDTVRRMM 240
DB 181 VGGIITRYAAVFGYVDTAKGMLPDPKXNTHIVVSMIAQTVAAGVVSYPEDTVRRMM 240
QY 241 OSGRKADIMYTGTLDCMRKIATDEGKAFKAGMSNVLRGAGAFVLYVDELKVI 298
DB 241 OSGRKADIMYTGTLDCMRKIATDEGKAFKAGMSNVLRGAGAFVLYVDELKVI 298

RESULT 3
ADT2 HUMAN
ID ADT2 HUMAN STANDARD; PRT; 298 AA.
AC POS141; 043350;
DT 13-AUG-1987 (Rel. 05; Created)
DT 01-OCT-1994 (Rel. 30; Last sequence update)
DT 28-FEB-2003 (Rel. 41; Last annotation update)
DE ADP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
DE SLC25A5 OR ANT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA MEDLINE=90375457; PubMed=2168878;
RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baezaga R., Muzel J.;
RT "The human fibroblast adenine nucleotide translocator gene. Molecular
RT cloning and sequence."
RL J. Biol. Chem. 265:16060-16063(1990).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=8716056; PubMed=3031073;
RA Battini R., Ferreri S., Kaczmarek L., Calabretta B., Chen S.T.,
RA Baezaga R.;
RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
RT growth-regulated."
RL J. Biol. Chem. 262:4355-4358(1987).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen C.N., Su Y., Baydayan P., Struno A., Nagaraia R.,
RA Mazarela R.A., Schlesinger D., Chen B.Y.;
RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Becker M., Graves T., Ozerky P.;
RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.
RN [5]
RP SEQUENCE OF 47-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houldsworth J., Attardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver."
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

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CC or send an email to license@isb-sib.ch).
CC -----
DB 241 OSGRKADIMYTGTLDCMRKIATDEGKAFKAGMSNVLRGAGAFVLYVDELKVI 296
CC EMBL; M57424; AAA51737.1; -
CC EMBL; J02683; AAA35579.1; -
CC EMBL; L78810; AAB39266.1; -
CC EMBL; AC004000; AAB6347.1; -
CC EMBL; J03591; AAA36749.1; -
CC PIR; A29132; A29132.
CC Genew; HGNC:10991; SLC25A5.
CC MIM; 300150; -
DR GO; GO:0005887; C:integral to plasma membrane; TMS.
DR GO; GO:0015207; F:adenine transporter activity; TMS.
DR GO; GO:0006832; P:small molecule transport; TMS.
DR InterPro; IPR002067; Mlt_carrier.
DR InterPro; IPR002030; Mlt_uncoupling.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mltc_carri; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSSEM 12 29
FT TRANSSEM 73 91
FT TRANSSEM 117 134
FT TRANSSEM 176 195
FT TRANSSEM 214 231
FT TRANSSEM 273 291
FT REPEAT 1 111
FT REPEAT 112 208
FT REPEAT 209 298
FT CONFLICT 6 6
FT CONFLICT 66 66
FT CONFLICT 111 111
FT CONFLICT 162 162
SQ SEQUENCE 298 AA; 32895 MM; P973C3AED92C49D3 CRC64;

Query Match 94.8%; Score 1463; DB 1; Length 298;
Best Local Similarity 92.9%; Pred. No. 3.8e-121;
Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 MTEQALSPADPLAGGIAAIAISKTAVALPIRKYLLGVHASKQIADKQYKGVDCIVR 60
DB 1 MTEQALSPADPLAGGIAAIAISKTAVALPIRKYLLGVHASKQIADKQYKGVDCIVR 60
QY 61 IPKEQVLSFWKGNLANVIRPPTOALNPAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120
DB 61 IPKEQVLSFWKGNLANVIRPPTOALNPAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDPARTRLADVKGSGTEREFGDCLVKTYSKGIRGLYOGFSVS 180
DB 121 GAAGATSLCFVYPLDPARTRLADVKGSGTEREFGDCLVKTYSKGIRGLYOGFSVS 180
QY 181 VGGIITRYAAVFGYVDTAKGMLPDPKXNTHIVVSMIAQTVAAGVVSYPEDTVRRMM 240
DB 181 VGGIITRYAAVFGYVDTAKGMLPDPKXNTHIVVSMIAQTVAAGVVSYPEDTVRRMM 240
QY 241 OSGRKADIMYTGTLDCMRKIATDEGKAFKAGMSNVLRGAGAFVLYVDELKVI 296
DB 241 OSGRKADIMYTGTLDCMRKIATDEGKAFKAGMSNVLRGAGAFVLYVDELKVI 296

RESULT 4
ADT2 RAT
ID ADT2 RAT STANDARD; PRT; 298 AA.
AC 009073;
DT 01-FEB-1995 (Rel. 31; Created)

```

DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DR ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
 DE (Adenine nucleotide translocator 2) (ANT 2).
 GN SLC25A5 OR ANT2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE-Liver;
 RX MEDLINE=94002161; PubMed=8399300;
 RA Shinohara Y., Kamada M., Yamazaki N., Terada H.;
 RT "Isolation and characterization of cDNA clones and a genomic clone
 encoding rat mitochondrial adenine nucleotide translocator.";
 RL Biochim. Biophys. Acta 1152:192-196 (1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND
 CC SKELETAL MUSCLE.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL, D12771; BAA02238.1; -
 DR InterPro; IPR002067; Mtc_carrier.
 DR InterPro; IPR002030; Mtc_uncoupling.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mto_carr; 3-
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00784; MITOCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 DR KX Mitochondriol; Inner membrane; Repeat; Transmembrane; Transport;
 KY Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32901 MW; 6A59204B987E9F35 CRC64;
 Query Match 94.0%; Score 1451; DB 1; Length 298;
 Best Local Similarity 91.9%; Pred. No. 4.3e-120;
 Matches 272; Conservative 15; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MTEQAI SPKADFLAGGIAAIAIKTAVAFERVKLLIQVHASKQIADQYGYDCTVR 60
 DB 1 MTDAAVSPAKDPLAGGVAAIAIKTAVAFERVKLLIQVHASKQIADQYGYDCTVR 60
 QY 61 IPEKGVSPFRGNLANVRYPTQALNFAFDKQYQIPLGGVDKHTQFWRFPAGNLASG 120
 DB 61 IPEKGVSPFRGNLANVRYPTQALNFAFDKQYQIPLGGVDKHTQFWRFPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFAFRLADVKGSGTEREFRGLGDLVYTKSDGIRGLYOGFSVS 180
 DB 121 GAAGATSLCFVYPLDFAFRLADVKGSGTEREFRGLGDLVYTKSDGIRGLYOGFSVS 180
 QY 122 GAAGATSLCFVYPLDFAFRLADVKGSGTEREFRGLGDLVYTKSDGIRGLYOGFSVS 180
 DB 122 GAAGATSLCFVYPLDFAFRLADVKGSGTEREFRGLGDLVYTKSDGIRGLYOGFSVS 180
 QY 181 VGGIITTYRAAYGVGVDTAAGMLPDPKNTHTIVVSMIAQTVTVAAGVVSFPFDTTTRRRMM 240

DB 181 VGGIITTYRAAYGVGVDTAAGMLPDPKNTHTIVVSMIAQTVTVAAGVVSFPFDTTTRRRMM 240
 QY 241 QSGRGADIMTYGVDCWRKIIFDEGKAFPGKASNYLRGNGAFVLYYDELK 296
 DB 241 QSGRGADIMTYGVDCWRKIIFDEGKAFPGKASNYLRGNGAFVLYYDELK 296
 RESULT 5
 ADT2 MOUSE
 ID ADT2 MOUSE STANDARD; PRT; 298 AA.
 AC P51881; O61311;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
 DE (Adenine nucleotide translocator 2) (ANT 2).
 GN SLC25A5 OR ANT2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=97059403; PubMed=8903724;
 RA Ellison J.W., Li X., Francke U., Shapiro J.J.;
 RT "Rapid evolution of human pseudautosomal genes and their mouse
 RT homologs.";
 RL Mamm. Genome 7:25-30 (1996).
 RN
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RA Sheldon J.G.;
 RT Sheils (1995), University of Cambridge, U.K.
 RN
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv;
 RA Costel P., Laplace C.;
 RT Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
 RN
 RN [4]
 RP REVISIONS.
 RA Laplace C.;
 RT Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20432087; PubMed=10974536;
 RA Levy S.B., Chen Y.-S., Graham B.H., Wallace D.C.;
 RT "Expression and sequence analysis of the mouse adenine nucleotide
 RT translocase 1 and 2 genes.";
 RL Gene 254:57-66 (2000).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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 CC -----
 DR EMBL, U27316; AAC52838.1; -
 DR EMBL, U10404; AAA19009.1; -
 DR EMBL, X70847; CAA50196.1; -
 DR EMBL, AF240003; AAF64471.1; -
 DR MGD; MGI:1353496; SLC25A5.
 DR InterPro; IPR002067; Mtc_carrier.

DR InterPro; IPR002030; Mit uncoupling.
 DR InterPro; IPR001993; Mitoch carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00784; MITOC CARRIER.
 DR PROSITE; PS00215; MITOCH CARRIER; 3.
 DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32931 MW; 0798B04B987E9E20 CRC64;

Query Match 93.6%; Score 1445; DB 1; Length 298;
 Best Local Similarity 91.6%; Pred. No. 1.4e-119;
 Matches 271; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTEQAISPAKDFLAGGIAAIASTKAVAPIERVKLLQVQHASKOIAADKQYKGIIVDCIVR 60
 DB 1 MTDAAVSPAKDFLAGGVAIASTKAVAPIERVKLLQVQHASKOITADKQYKGIIVDCIVR 60
 QY 61 IPKQGVLSFWRGKLANVIRFPFOALNPAFKDKYKQIFLGVDKHTQFMWYFAGNLASG 120
 DB 61 IPKQGVLSFWRGKLANVIRFPFOALNPAFKDKYKQIFLGVDKHTQFMWYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDPFARTRLAADVGKSGTEREFGGLDCLVTKSGDGLGKQGFVS 180
 DB 121 GAAGATSLCFVYPLDPFARTRLAADVGKSGTEREFGGLDCLVTKSGDGLGKQGFVS 180
 QY 181 VQGIITRYAAVFGVYDTAKGMLPDPKXTHIVSWMIAQTVAAGVVSYPDTRRRMM 240
 DB 181 VQGIITRYAAVFGVYDTAKGMLPDPKXTHIVSWMIAQTVAAGVVSYPDTRRRMM 240
 QY 241 QSGRGKADIMYTGVDICWRKIIFRDEGKAFPGKAMSVNLKMGAFVLVYDELK 296
 DB 241 QSGRGKADIMYTGVDICWRKIIFRDEGKAFPGKAMSVNLKMGAFVLVYDELK 296

RESULT 6
 ADT1 RAT STANDARD; PRT; 298 AA.

AC Q05962;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
 DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
 GN SL25A4 OR ANT1.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley, and Wistar; TISSUE=Heart, and Liver;
 RX MEDLINE=94002161; PubMed=8399300;
 RA Shinohara Y., Kamida M., Yamazaki N., Terada H.;
 RT "Isolation and characterization of cDNA clones and a genomic clone
 RT encoding rat mitochondrial adenine nucleotide translocator";
 RL Biochem. Biophys. Acta 1152:192-196(1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER
 CC EXTENT, IN BRAIN AND KIDNEY.

CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC
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 CC or send an email to license@ebi.ac.uk).

DR EMBL; X61667; CA43842.1; -;
 DR EMBL; D12770; BAA0237.1; -;
 DR PIR; I60173; I60173.
 DR InterPro; IPR002067; Mit carrier.
 DR InterPro; IPR002030; Mit uncoupling.
 DR InterPro; IPR001993; Mitoch carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00784; MITOCH CARRIER; 3.
 DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32989 MW; 66704F786C320 CRC64;

Query Match 92.3%; Score 1424; DB 1; Length 298;
 Best Local Similarity 89.6%; Pred. No. 1e-117;
 Matches 267; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEQAISPAKDFLAGGIAAIASTKAVAPIERVKLLQVQHASKOIAADKQYKGIIVDCIVR 60
 DB 1 MGDQALSFLLKDFLAGGIAAIASTKAVAPIERVKLLQVQHASKOISAEKQYKGIIVDCIVR 60
 QY 61 IPKQGVLSFWRGKLANVIRFPFOALNPAFKDKYKQIFLGVDKHTQFMWYFAGNLASG 120
 DB 61 IPKQGVLSFWRGKLANVIRFPFOALNPAFKDKYKQIFLGVDKHTQFMWYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDPFARTRLAADVGKSGTEREFGGLDCLVTKSGDGLGKQGFVS 180
 DB 121 GAAGATSLCFVYPLDPFARTRLAADVGKSGTEREFGGLDCLVTKSGDGLGKQGFVS 180
 QY 181 VQGIITRYAAVFGVYDTAKGMLPDPKXTHIVSWMIAQTVAAGVVSYPDTRRRMM 240
 DB 181 VQGIITRYAAVFGVYDTAKGMLPDPKXTHIVSWMIAQTVAAGVVSYPDTRRRMM 240
 QY 241 QSGRGKADIMYTGVDICWRKIIFRDEGKAFPGKAMSVNLKMGAFVLVYDELK 298
 DB 241 QSGRGKADIMYTGVDICWRKIIFRDEGKAFPGKAMSVNLKMGAFVLVYDELK 298

RESULT 7

ADT1 MOUSE STANDARD; PRT; 298 AA.
 AC P48962; Q62164;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE ADP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
 DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1) (MANC1).
 GN SL25A4 OR ANT1 OR ANCI.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;

[1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6; TISSUE=Brain;
 RC MEDLINE=97059403; PubMed=8903724;
 RX Ellison J.W., Li X., Francke U., Shapiro L.J.;
 RA "Rapid evolution of human pseudocautosomal genes and their mouse
 homologs.";
 RT Mamm. Genome 7:25-30(1996).
 RL
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Muscle;
 RA Laplace C., Costet P.;
 RL Submitted (SEP-1993) to the EMBL/Genbank/DBJ databases.
 RN
 RP SEQUENCE FROM N.A.
 [3]
 RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
 RT "Expression and sequence analysis of the mouse adenine nucleotide
 translocase 1 and 2 genes.";
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 RN
 RP SEQUENCE FROM N.A.
 [4]
 RC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheefter C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Cantucci P., Pearce C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
 RA Boeck S.A., McEwen P.J., McKernan K.U., Malek J.A., Gnaratne P.H.,
 RA Richards S., Wotley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schultz J., Myers R.W.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.B.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN
 RP
 RT
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC
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 CC
 CC
 CC EMBL, U27315; AAC52837.1; -
 CC EMBL, X74510; CAAS2616.1; -
 CC EMBL, AF240002; AAF64470.1; -
 CC EMBL, BC003791; AAH03791.1; -
 CC EMBL, BC026925; AAH26925.1; -
 CC PIR, S37210; S37210.
 CC MGI, MGI:1353495; Slc25a4.
 CC InterPro, IPR002067; Mlt_carrier.
 CC InterPro, IPR002030; Mlt_uncoupling.
 CC InterPro, IPR001993; Mltch_carrier.
 CC Pfam, PF00153; mltc_car; 3 -
 CC PRINTS, PR00926; MITOCARRIER.
 CC PRINTS, PR00784; MTUNCOUPLING.
 CC PROSITE, PS00215; MITOCH_CARRIER; 3.

KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 208 2.
 FT REPEAT 209 298 3.
 FT CONFLICT 136 136 F -> L (IN REF. 1).
 SQ SEQUENCE 298 AA; 32904 MM; 3A849FEA0981462 CAC64;
 Query Match 91.9%; Score 1418; DB 1; Length 298;
 Best Local Similarity 88.9%; Pred. 3.4e-117;
 Matches 265; Conservative 19; Mismatches 14; Indels 0; Gaps 0;
 QY 1 MTEQALSPKRPFLAGIAAIASTKRAVPIERVKLLQVQHSKQIAADKQKGIYDCTVR 60
 DB 1 MGDDALSPDKDFLAGIAAASKTAIVPIERVKLLQVQHSKQISAKQYKGIIDCVVR 60
 QY 1PKKGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFMRYFAGNLASG 120
 DB 61 IPKGGFSLFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFMRYFAGNLASG 120
 QY 121 GAAGATSLCFYYPPLDPARTRLAADVGKSGTEREFGGLDCLVKTSGIRGLYQGFSSVS 180
 DB 121 GAAGATSLCFYYPPLDPARTRLAADVGKSGTEREFGGLDCLVKTSGIRGLYQGFSSVS 180
 QY 181 VGGIITTYAAAFYGVYDPTAKGMLPDKNTHIVSWMIQTVYAVAGVSYPPDTPRRMM 240
 DB 181 VGGIITTYAAAFYGVYDPTAKGMLPDKNTHIVSWMIQTVYAVAGVSYPPDTPRRMM 240
 QY 241 QSGRKGADIMVTGTVDCKRKIFRDEGKAFPKGAMSVTLRGGAFLVLYDELTKVI 298
 DB 241 QSGRKGADIMVTGTVDCKRKIAKDEGANAFPKGAMSVTLRGGAFLVLYDELTKVI 298
 RESULT 8
 ID ADP1 BOVIN STANDARD; PRT; 297 AA.
 AC P02722;
 DT 21-JUN-1986 (Rel. 01, Created)
 DT 01-JUN-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP/ATP carrier protein, heart isoform T1 (ADP/ATP translocase 1)
 DE (Adenine nucleotide translocator 1) (ANT 1).
 GN SLIC25A4 OR ANT1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN
 RP SEQUENCE FROM N.A.
 RP MEDLINE=89229093; PubMed=2540808;
 RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
 RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
 RT differences in various tissues.";
 RL Biochemistry 28:866-873(1989).
 RN
 RP SEQUENCE.
 RP MEDLINE=82188267; PubMed=7076130;
 RA Aquila H., Misra D., Rulicz M., Kligenberg M.;
 RT "Complete amino acid sequence of the ADP/ATP carrier from beef heart
 RT mitochondria.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 363:345-349(1982).
 RN
 RP SEQUENCE OF 207-297 FROM N.A.
 RP MEDLINE=86295775; PubMed=3017341;
 RA Rasmussen U.B., Wohlrab H.;
 RT "Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and

RT an unusually short 3'-noncoding sequence.";
 RL Blochem. Biophys. Res. Commun. 138:850-857(1986).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC
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DR EMBL: M13783; AAA0363.1; -;
 DR EMBL: M24102; AAA0768.1; -;
 DR PIR: A43646; XMOO.
 DR InterPro: IPR002067; Mit carrier.
 DR InterPro: IPR002030; Mit uncoupling.
 DR InterPro: IPR001993; Mitoch carrier.
 DR Pfam: PF00153; mito carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Mitochondion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family; Methylolacton.
 FT INIT MET 0 0
 FT MOD_RES 1 1 BLOCKED
 FT TRANSMEM 51 51 METHYLATION (POTENTIAL).
 FT TRANSMEM 11 28 1 (POTENTIAL).
 FT TRANSMEM 72 90 2 (POTENTIAL).
 FT TRANSMEM 116 133 3 (POTENTIAL).
 FT TRANSMEM 175 194 4 (POTENTIAL).
 FT TRANSMEM 213 230 5 (POTENTIAL).
 FT TRANSMEM 272 290 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 207 2.
 FT REPEAT 208 297 3.
 SQ SEQUENCE 297 AA; 32836 MW; A582D3C4A40A8B48 CMC64;

Query Match 91.8%; Score 1417; DB 1; Length 297;
 Best Local Similarity 89.2%; Pred. NO. 4.1e-117;
 Matches 265; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 2 TEONISPAKDFLAGIAAIAIKTAVAPERYKLLVOHASKOIAADKQYGVDCVIRI 61
 DB 1 SDQSLSEKDFLAGVAAIAIKTAVAPERYKLLVOHASKOIAADKQYGVDCVIRI 60
 QY 62 PKEGVSLFWRGNLANVIRYPTOLNFAFDKTKQIFLGVDVHQTQFWRYFAGNLASGG 121
 DB 61 PKEGVSLFWRGNLANVIRYPTOLNFAFDKTKQIFLGVDVHQTQFWRYFAGNLASGG 120
 QY 122 AAGATSLCTFPVLPDPAFTRIALADVKGSGTEREFGDCLVTKTSQIRGLYQGSVSU 181
 DB 121 AAGATSLCTFPVLPDPAFTRIALADVKGSGTEREFGDCLVTKTSQIRGLYQGSVSU 180
 QY 182 OGIIYAAVGVYDPAKGMEDPKNTHTIVVSMIAQVTVAVAGVSPPTVARRMMQ 241
 DB 181 OGIIYAAVGVYDPAKGMEDPKNTHTIVVSMIAQVTVAVAGVSPPTVARRMMQ 240
 QY 242 SGRKADIMTYGVDCWRKIFRDEGKAFFKAGSNVLRGGAFAVLVYDELKVI 298
 DB 241 SGRKADIMTYGVDCWRKIFRDEGKAFFKAGSNVLRGGAFAVLVYDELKVI 297

RESULT 9
 ADTI HUMAN
 ID ADTI HUMAN STANDARD; PRT; 298 AA.
 AC P12235;

DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
 DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
 GN SLC25A4 OR ANT1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89236396; PubMed=2541251;
 RA Corone A.L., Runswick M.J., Walker J.E.;
 RT "DNA sequences of two expressed nuclear genes for human mitochondrial
 RT ADP/ATP translocase.";
 RL J. Mol. Biol. 206:261-280(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89340499; PubMed=2547778;
 RA Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,
 RA Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;
 RT "A human muscle adenine nucleotide translocator gene has four exons,
 RT is located on chromosome 4, and is differentially expressed.";
 RL J. Biol. Chem. 264:13998-14004(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88041149; PubMed=2823266;
 RA Neukelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;
 RT "cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack
 RT of a leader peptide, divergence from a fibroblast translocator cDNA,
 RT and coevolution with mitochondrial DNA genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92388257; PubMed=12477932;
 RA Strausberg R.L., Pelngold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Ueidi T.B., Toshiki S., Canninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Holtz E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalek U., Small D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Maria M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 1-37 FROM N.A.
 RX MEDLINE=88124845; PubMed=2829183;
 RA Houldsworth J., Altardi G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
 RT level in adult human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
 RN [6]
 RP VARIANTS PRO PRO-114 AND MET-289.
 RX MEDLINE=20385067; PubMed=10926541;
 RA Kaukonen J., Juselius J.K., Tiraniti V., Kyttala A., Zeviani M.,
 RA Comi G.P., Keranen J., Peltonen L., Suomalainen A.;
 RT "Role of adenine nucleotide translocator 1 in mtDNA maintenance.";
 RL Science 289:782-785(2000).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE

CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC progressive external ophthalmoplegia with various mitochondrial
 CC DNA deletions (PEO). Patients with PEO have mitochondrial
 CC myopathy, progressive external ophthalmoplegia, and other
 CC abnormalities associated with multiple different deletions of
 CC mitochondrial DNA.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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 CC DR EMBL; J02966; AAA61223.1; -.
 CC DR EMBL; J03593; AAA56751.1; -.
 CC DR EMBL; J04982; AAA51736.1; -.
 CC DR EMBL; BC008664; AAH08664.1; -.
 CC DR PIR; A44778; A44778.
 CC DR Genem; HGNC:10990; SLC25A4.
 CC DR MIM; 103220; -.
 CC DR MIM; 157640; -.
 CC DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC DR GO; GO:0005739; C:mitochondrion; TAS.
 CC DR GO; GO:0015207; P:adenine transporter activity; TAS.
 CC DR GO; GO:0006091; P:energy pathways; TAS.
 CC DR GO; GO:0000002; P:mitochondrial genome maintenance; TAS.
 CC DR GO; GO:0006832; P:small molecule transport; TAS.
 CC DR InterPro; IPR002067; Mtc_carrier.
 CC DR InterPro; IPR020303; Mtc_uncoupling.
 CC DR InterPro; IPR001993; Mitoch_carrier.
 CC DR Pfam; PF00153; mto_carr; 3.
 CC DR PRINTS; PR00926; MITOCARRIER.
 CC DR PRINTS; PR00784; MTNCOUPLING.
 CC DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 CC DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 CC MultiGene family; Disease mutation.
 CC KW TRANSMEM 12 29 1 (POTENTIAL).
 CC FT TRANSMEM 73 91 2 (POTENTIAL).
 CC FT TRANSMEM 117 134 3 (POTENTIAL).
 CC FT TRANSMEM 176 195 4 (POTENTIAL).
 CC FT TRANSMEM 214 231 5 (POTENTIAL).
 CC FT TRANSMEM 273 291 6 (POTENTIAL).
 CC FT REPEAT 1 110 1.
 CC FT REPEAT 111 208 2.
 CC FT REPEAT 209 298 3.
 CC FT VARIANT 114 114 A->P (IN PEO).
 CC FT VARIANT 289 289 /FTID=VAR_012111.
 CC FT VARIANT 289 289 V->M (IN PEO).
 CC FT CONFLICT 16 16 /FTID=VAR_012112.
 CC FT CONFLICT 147 149 G->A (IN REF. 3).
 CC FT CONFLICT 227 227 KCA->R (IN REF. 3).
 CC FT CONFLICT 227 227 V->L (IN REF. 3).
 CC SQ SEQUENCE 298 AA; 33064 MW; 59F0DPRACAE7CFBB CRC64;
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 CC Query Match 91.3%; Score 1409; DB 1; Length 298;
 CC Best Local Similarity 88.3%; Pred. No. 2.1e-116;
 CC Matches 263; Conservative 19; Mismatches 16; Indels 0; Gaps 0;
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 CC QY 1 MTEQASIPKQFLAGIAAISTKVAIPERVKLLQVQHASKQIADKQYGIYDQVR 60
 CC DB 1 MGDHMSFLKDFLAGVAANAASKTVAIPERVKLLQVQHASKQIADKQYGIYDQVR 60
 CC QY 1 PKKGVSLSPKRGNIANTYRPFQALNAPFKDKTKQIFLGVDVGHGTQFWREAGNLASG 120
 CC DB 1 PKKGVSLSPKRGNIANTYRPFQALNAPFKDKTKQIFLGVDVGHGTQFWREAGNLASG 120

QY 121 GAAGATSLCFYYPIDPAFTRLAADVSGSTEREERGLDCLVTKTSGDINGLYOGFSVS 180
 DB 121 GAAGATSLCFYYPIDPAFTRLAADVSGSTEREERGLDCLVTKTSGDINGLYOGFSVS 180
 QY 181 VGGIITVYAAAFYGVDTKQMLPDKNTHIVSWNMIACTVAVGVSYPPDYRRMM 240
 DB 181 VGGIITVYAAAFYGVDTKQMLPDKNTHIVSWNMIACTVAVGVSYPPDYRRMM 240
 QY 241 QSGRGKADIMYTGVDGCRKIFRDEGKAFKFGKAMSVNLRGGAFFVLYDELKRV 298
 DB 241 QSGRGKADIMYTGVDGCRKIFRDEGKAFKFGKAMSVNLRGGAFFVLYDELKRV 298
 RESULT 10
 ADT DROME STANDARD; PRT; 299 AA.
 AC 026365; P91614; Q26254; Q95S30; Q9VZ70;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE ADP-ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
 DE translocator) (ANT) (Stress sensitive B protein).
 GN SEB OR A/A-T OR CG16944.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_Taxid=7227;
 OX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92389367; Pubmed=1387687;
 RA Louvi A., Tsiftoglou S.G.;
 RT "A cDNA clone encoding the ADP/ATP translocase of Drosophila
 RT melanogaster shows a high degree of similarity with the mammalian
 RT ADP/ATP translocases".
 RL J. Mol. Evol. 35:44-50(1992).
 RL [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94350065; Pubmed=7520869;
 RA Hutter P., Karch F.;
 RT "Molecular analysis of a candidate gene for the reproductive
 RT isolation between sibling species of Drosophila".
 RL Experientia 50:749-762(1994).
 RL [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Oregon-R;
 RA Zhang Y.Q., Davis A.W., Roote J., Herrmann S., Ashburner M.;
 RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
 RL [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; Pubmed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.-H.C., Blazek R.G., Chapple M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Barker E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Abghyan A.A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Baas A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burtis K.C., Buam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Clacher A., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Duthin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabrielian A.B., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glisdek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegwam C.,
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang X., Lin X.,
 RA Liu X., Maitel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mekulov G., Misha N.V., Mobarry C., Morris J., Mosher A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacle J.M.,
 RA Palazolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shie B.C., Siden-Kimmo I., Simpson M., Skupski M.P., Smith T.,
 RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195 (2000).
 [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley; TISSUE=larva, Ovary, and Pupae;
 RX MEDLINE=22426066; PubMed=12537569;
 RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champagne M.,
 RA George R.A., Guarini H., Krommiller B., Pacle J.M., Park S., Wan K.H.,
 RA Rubin G.M., Celniker S.E.;
 RT "A *Drosophila* full-length cDNA resource.";
 RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8 (2002).
 CC -1- FUNCTION: Catalyzes the exchange of ADP and ATP across the
 CC mitochondrial inner membrane.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane (By similarity).
 CC -1- DOMAIN: Composed of three homologous domains.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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 CC -----
 CC EMBL; S43651; AAB23114.1; -;
 DR EMBL; S71762; AAB31734.3; -;
 DR EMBL; Y10618; CA471628.1; -;
 DR EMBL; AB003484; AAF47957.1; -;
 DR EMBL; AY060978; AAL28526.1; -;
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 DR FLYBase; FBgn000360; seeb.
 DR GO; GO:0005743; C:mitochondrial inner membrane; IMP.
 DR GO; GO:0006839; P:mitochondrial transport; IMP.
 DR InterPro; IPR002067; Mlt carrier.
 DR InterPro; IPR001993; Mitoch carrier.
 DR Pfam; PF00153; mito_carr; 2;
 DR PRINTS; PRO0926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
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 FT TRANSMEM 4611 4629 125 (POTENTIAL).
 FT TRANSMEM 4647 4665 126 (POTENTIAL).
 FT TRANSMEM 4683 4701 127 (POTENTIAL).
 FT TRANSMEM 4719 4737 128 (POTENTIAL).
 FT TRANSMEM 4755 4773 129 (POTENTIAL).
 FT TRANSMEM 4789 4807 130 (POTENTIAL).
 FT TRANSMEM 4825 4843 131 (POTENTIAL).
 FT TRANSMEM 4861 4879 132 (POTENTIAL).
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 FT TRANSMEM 4933 4951 134 (POTENTIAL).
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 FT TRANSMEM 5041 5059 137 (POTENTIAL).
 FT TRANSMEM 5077 5095 138 (POTENTIAL).
 FT TRANSMEM 5113 5131 139 (POTENTIAL).
 FT TRANSMEM 5149 5167 140 (POTENTIAL).
 FT TRANSMEM 5185 5203 141 (POTENTIAL).
 FT TRANSMEM 5221 5239 142 (POTENTIAL).
 FT TRANSMEM 5257 5275 143 (POTENTIAL).
 FT TRANSMEM 5293 5311 144 (POTENTIAL).
 FT TRANSMEM 5329 5347 145 (POTENTIAL).
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 FT TRANSMEM 5469 5487 149 (POTENTIAL).
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 FT TRANSMEM 7113 7131 195 (POTENTIAL).
 FT TRANSMEM 7149 7167 196 (POTENTIAL).
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 FT TRANSMEM 10329 10347 285 (POTENTIAL).
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 FT TRANSMEM 10577 10595 292 (POTENTIAL).
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 FT TRANSMEM 10685 10703 295 (POTENTIAL).
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 FT TRANSMEM 12613 12631 349 (POTENTIAL).
 FT TRANSMEM 12649 12667 350 (POTENTIAL).
 FT TRANSMEM 12685 12703 351 (POTENTIAL).
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 FT TRANSMEM 12793 12811 354 (POTENTIAL).
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 FT TRANSMEM 13077 13095 362 (POTENTIAL).
 FT TRANSMEM 13113 13131 363 (POTENTIAL).
 FT TRANSMEM 13149 13167 364 (POTENTIAL).
 FT TRANSMEM 13185 13203 365 (POTENTIAL).
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 FT TRANSMEM 13257 13275 367 (POTENTIAL).
 FT TRANSMEM 13293 13311 368 (POTENTIAL).
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 FT TRANSMEM 13757 13775 381 (POTENTIAL).
 FT TRANSMEM 13793 13811 382 (POTENTIAL).
 FT TRANSMEM 13829 13847 383 (POTENTIAL).
 FT TRANSMEM 13865 13883 384 (POTENTIAL).

Query Match
Best Local Similarity 77.7%; Pred. No. 2.1e-98;
Matches 233; Conservative 23; Mismatches 42; Indels 2; Gaps 1;

Query 1 MTEQA--ISFADFLAGGIAAISTKAVAPIERVKLLQVQASQIADKQKGIIVDCI 58
Db 1 MTKKADPRGFADPLAGGSAVSKTAVPIERVKLLQVQASQIADKQKGIIVDCI 60

Query 59 VRIPEQGLVSWRGNLANVIRFPLOALNFAFKDKYKQIFLGVDKHTQFRRYAGNIA 118
Db 61 VRIPEQGLVSWRGNLANVIRFPLOALNFAFKDKYKQIFLGVDKHTQFRRYAGNIA 120

Query 119 SGGAAGATSLCFVYPLDPAFRTLAADVGSCTEREPRGIDCLVKTISDGIKGIYQGS 178
Db 121 SGGAAGATSLCFVYPLDPAFRTLAADVGSCTEREPRGIDCLVKTISDGIKGIYQGS 180

Query 179 VSVQGIITIRAYAFGVYDTAKGMLDPPKNTHTIVSWMTAQVTAVAGVSYEPDTRRRM 238
Db 181 VSVQGIITIRAYAFGVYDTAKGMLDPPKNTHTIVSWMTAQVTAVAGVSYEPDTRRRM 240

Query 239 MWQGRKADIMYTGTVDCWRKIFRDEGKAFPKGAMSNVLRGMGAFLVLYDELKQVI 298
Db 241 MWQGRKADIMYTGTVDCWRKIFRDEGKAFPKGAMSNVLRGMGAFLVLYDELKQVI 300

RESULT 12
ID ADT CHLKE STANDARD; PRT; 339 AA.

AC P31692;
DT 01-JUN-1993 (Rel. 26, Last sequence update)
DT 01-JUN-1993 (Rel. 26, Last annotation update)
DE 15-OUT-1998 (Rel. 36, Last annotation update) (Adenine nucleotide translocator) (ANT).
OS Chlorella kessleri.
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales; Chlorellaceae; Chlorella.
CC NCBI_TaxID=3074;
NN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92084708; PubMed=1748677;
RA Hilgarch C., Sauer N., Tanner W.;
RT "Glucose increases the expression of the ATP/ADP translocator and the glyceraldehyde-3-phosphate dehydrogenase genes in Chlorella.";
RL J. Biol. Chem. 266:24044-24047(1991).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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CC -----
CC EMBL, M76669; AAA33027.1; -;
CC PIR, A41677; A41677.
CC InterPro, IPR002067; Mlt carrier.
CC InterPro, IPR001993; Mitoch carrier.
CC Pfam, PF00153; mltc carr; 3-
CC PRINTS, PR00926; MITOCARRIER.
CC PROSITE, PS00215; MITOCH_CARRIER; 3.

Query Match
Best Local Similarity 63.4%; Score 978; DB 1; Length 339;
Matches 198; Conservative 26; Mismatches 64; Indels 8; Gaps 5;

Query 6 ISFADFLAGGIAAISTKAVAPIERVKLLQVQASQIADK--QYKGIIVDCI 63
Db 39 MAFVLDLAGGTAGASISTKAVAPIERVKLLQVQASQIADK--QYKGIIVDCI 98

Query 64 EGVLSFWRGNLANVIRFPLOALNFAFKDKYKQIFLGVDKHTQFRRYAGNIA 123
Db 99 EGVLSFWRGNLANVIRFPLOALNFAFKDKYKQIFLGVDKHTQFRRYAGNIA 157

Query 124 GATSLCFVYPLDPAFRTLAADVGSCTEREPRGIDCLVKTISDGIKGIYQGS 183
Db 158 GATSLCFVYPLDPAFRTLAADVGSCTEREPRGIDCLVKTISDGIKGIYQGS 216

Query 184 IIRAYAFGVYDTAKGMLDPPKNTHTIVSWMTAQVTAVAGVSYEPDTRRRM 242
Db 217 IIRAYAFGVYDTAKGMLDPPKNTHTIVSWMTAQVTAVAGVSYEPDTRRRM 276

Query 243 GRKADIMYTGTVDCWRKIFRDEGKAFPKGAMSNVLRGMGAFLVLYDELKQVI 298
Db 277 GRKADIMYTGTVDCWRKIFRDEGKAFPKGAMSNVLRGMGAFLVLYDELKQVI 329

RESULT 13
ID ADT3 YEAST STANDARD; PRT; 307 AA.

AC P16238;
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE 01-OCT-1994 (Rel. 30, Last annotation update)
DE ADP carrier protein 3 (ADP/ATP translocator 3) (Adenine nucleotide translocator 3) (ANT 3).
GN AAC3 OR YBR085W OR YBR0753.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
CC NCBI_TaxID=4932;
NN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90324269; PubMed=2165073;
RA Kolarov J., Kolarova N., Nelson N.;
RT "A third ADP/ATP translocator gene in yeast.";
RL J. Biol. Chem. 265:12711-12716(1990).
CC [2]
RP SEQUENCE FROM N.A.
RX STRAIN=S288c;
RA Andre B., Cziepluch C., Hein C., Jauniaux J.C., Ureastarazu A.,
RS Viessers S.;
RT Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
CC [3]
RP SEQUENCE OF 38-307 FROM N.A.
RX Feldmann H., Mannhaupt G., Schwarzlouse C., Vetter I.;
RT Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -----

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CC or send an email to license@isb-sib.ch).

DR EMBL; M34076; AAA97485.1; -
DR EMBL; Z35954; CAA85031.1; -
DR PIR; A36582; A36582.
DR SGO; S0000289; AAC3.
DR SGO; GO:0005471; F:ATP/ADP antiporter activity; IMP.
DR GO; GO:0006854; P:ATP/ADP exchange; IMP.
DR InterPro; IPR002067; Mlt_carrier.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mltc_car; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 2.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 16 33 1 (POTENTIAL).
FT TRANSMEM 78 96 2 (POTENTIAL).
FT TRANSMEM 120 137 3 (POTENTIAL).
FT TRANSMEM 181 200 4 (POTENTIAL).
FT TRANSMEM 220 237 5 (POTENTIAL).
FT TRANSMEM 276 294 6 (POTENTIAL).
SQ SEQUENCE 307 AA; 33313 MW; D0C1329FECLBDC8 CRC64;

Query Match 50.5%; Score 778.5; DB 1; Length 307;
Best Local Similarity 53.7%; Pred. No. 4.5e-61;
Matches 161; Conservative 45; Mismatches 85; Indels 9; Gaps 5;

QY 3 EQAISPANQFLAGGIAAISTAVPIERVKLLQVQ-HASKQIADKQYKGIYDQIVRI 61
DB 7 QOETNFANFLMGVSAIAIAKTAASPIERVKILLIQODEMIKQGTLDKRYSGIYDQCFKRT 66
QY 62 PKEGVGSFWRGNLANVIRYPTQALNFAFKQYKQIPLGVDKHTQFWRYPAGNLASGG 121
DB 67 AKQEBLSFWRGNLANVIRYPTQALNFAFKQYKQIPLGVDKHTQFWRYPAGNLASGG 124
QY 122 AAGATSLCEVYPLDPAFRTLAADV--GKSGTERBERGGLDCLVKTSGDGRGLYQGSFV 179
DB 125 AAGATSLCEVYPLDPAFRTLAADV--GKSGTERBERGGLDCLVKTSGDGRGLYQGSFV 184
QY 180 SVGGIIIRAAVFGVYDTAKEM-LPDPKNTIIVSWMLAQTVTAAGVAVSYPFDTVRBM 238
DB 185 SVGGIIIRAAVFGVYDTAKEM-LPDPKNTIIVSWMLAQTVTAAGVAVSYPFDTVRBM 244
QY 239 MMOSGRKADIMYGTVDQWCKRIFRDBGCKAFPGKANSNVLRMGAGAVLVLYBELKVI 298
DB 245 MMTSGQA--VKYNGALDCLKRTIVASEGVSLFKGCGANILRSVAGAVISMTDQLMITL 301

RESULT 14
ADT_CHLRE STANDARD; PRT; 308 AA.
AC P27080;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE ADP carrier protein (ADP/ATP translocase) (Adenine nucleotide
translocator) (ANT).
GN ABL.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N. A.
RC STRAIN=FUD44-R2;
RX MEDLINE=93204887; PubMed=8455552;
RA Sharpe J. A., Day A.;

RT "Structure, evolution and expression of the mitochondrial ADP/ATP
RT translocator gene from Chlamydomonas reinhardtii.";
RL Mol. Gen. Genet. 237:134-144(1993).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRION INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC
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CC or send an email to license@isb-sib.ch).

DR EMBL; X65194; CAA46311.1; -
DR PIR; S30259; S30259.
DR InterPro; IPR002067; Mlt_carrier.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mltc_car; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 2.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 74 92 2 (POTENTIAL).
FT TRANSMEM 116 133 3 (POTENTIAL).
FT TRANSMEM 178 197 4 (POTENTIAL).
FT TRANSMEM 217 234 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
SQ SEQUENCE 308 AA; 33528 MW; D477CF0E72B7A53F CRC64;

Query Match 50.0%; Score 772; DB 1; Length 308;
Best Local Similarity 51.8%; Pred. No. 1.7e-60;
Matches 157; Conservative 55; Mismatches 81; Indels 10; Gaps 5;

QY 1 MTEQAISPANQFLAGGIAAISTAVPIERVKLLQVQ-HASKQIADKQYKGIYDQIVRI 59
DB 1 MAKEKKNMVDVFLAGSAVASTAAPIERVKILLIQODEMIKQGTLDKRYSGIYDQCFKRT 60
QY 60 RIPEQGVLSWRGNLANVIRYPTQALNFAFKQYKQIPLGVDKHTQFWRYPAGNLAS 119
DB 61 RIPEQGVLSWRGNLANVIRYPTQALNFAFKQYKQIPLGVDKHTQFWRYPAGNLAS 118
QY 120 GGAAGATSLCEVYPLDPAFRTLAADV--VGKSGTERBERGGLDCLVKTSGDGRGLYQGSFV 176
DB 119 GGAAGATSLCEVYPLDPAFRTLAADV--VGKSGTERBERGGLDCLVKTSGDGRGLYQGSFV 178
QY 177 FSVSVGGIIIRAAVFGVYDTAKEM-LPDPKNTIIVSWMLAQTVTAAGVAVSYPFDTVR 235
DB 179 FSVSVGGIIIRAAVFGVYDTAKEM-LPDPKNTIIVSWMLAQTVTAAGVAVSYPFDTVR 238
QY 236 RRMMSGRKADIMYGTVDQWCKRIFRDBGCKAFPGKANSNVLRMGAGAVLVLYBELK 295
DB 239 RRMMSGRKADIMYGTVDQWCKRIFRDBGCKAFPGKANSNVLRMGAGAVLVLYBELK 295
QY 296 KVI 298
DB 296 VIL 298

RESULT 15
ADT_SCHPO STANDARD; PRT; 322 AA.
AC Q09188;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADP carrier protein (ADP/ATP translocase) (Adenine nucleotide
translocator) (ANT).
GN ABL.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N. A.
RC STRAIN=FUD44-R2;
RX MEDLINE=93204887; PubMed=8455552;
RA Sharpe J. A., Day A.;

GN ANCI OR SPBC530.10C.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 OC NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=96257204; PubMed=8675018;
 RA Coulin N., Trezeguet V., Saux A.L., Lauguin G.J.M.;
 RT "Cloning of the gene encoding the mitochondrial adenine nucleotide
 carrier of Schizosaccharomyces pombe by functional complementation in
 Saccharomyces cerevisiae.";
 RL Gene 171:113-117(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holtroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagsle K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeli C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Wolchert G., Aert R., Robben J., Gymnopre B.,
 RA Wellens J., Vansteleels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leinrich H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Leleau V., Mottier S.,
 RA Gilbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.W.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Useery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880(2002).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer (by similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation-
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Z49974; CAA90275.1; -;
 CC EMBL; AL023634; CAA19176.1; -;
 CC PIR; T40526; T40526.
 CC GeneDB SPombe; SPBC530.10C; -;
 CC InterPro; IPR002067; Mtc_carrier.
 CC InterPro; IPR001993; Mitoch_carrier.
 CC Pfam; PF00153; mito_carr; 3.
 CC PRINTS; PR00926; MITOCARRIER.
 CC PROSITE; PS00215; MITOCH_CARRIER; 2.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 28 48 1
 FT TRANSMEM 93 111 2 (POTENTIAL).

FT TRANSMEM 131 151 3 (POTENTIAL).
 FT TRANSMEM 197 217 4 (POTENTIAL).
 FT TRANSMEM 222 242 5 (POTENTIAL).
 FT TRANSMEM 289 309 6 (POTENTIAL).
 SQ SEQUENCE 322 AA; 35020 MW; 8AC3D16A40F41AFC CRC64;
 Query Match 49.8%; Score 769; DB 1; Length 322;
 Best Local Similarity 53.6%; Pred. No. 3.3e-60;
 Matches 158; Conservative 50; Mismatches 75; Indels 12; Gaps 6;
 QY 7 SPADFLAGIAAIAISKTAIVPIREVKLLQVQHSKQIADK--QYGIYDQIVRIIPK 63
 DB 26 TFFPDPFMGVSAAVSKTAAPRIERYKLLIQN--DEIIRAGRSHRKAGIGECKRTAA 83
 QY 64 EGVLSFWRGMLAVIRYPTQALNPAFKDYKQIFLGVDKHTQFMRYFAGNTASGAA 123
 DB 84 EGVLSLWRGNTAVNLRFPQALNPAFKDKFKMF--GKKERDQYAKFAGNTASGAA 142
 QY 124 GATSLCFYPIIDFARTLAADV--GKSTEREPRGLGCLVKITSDGIRGLYGFSTVS 181
 DB 143 GAASLLFVYSIDYARTRLANDAKSAKKGKGFNGLVVYRKYRSDGLRGLYRFGPSV 202
 QY 182 QGIIYRAYRGVVDYTAGK-MLPDKQTHIVSMWIAQVTAAGVVSYPDQVRRBMM 240
 DB 203 VGIVYRGLYGMVDLKPVLVGLBGNFLASFLGNAVTTGSGVASYPDQVRRBMM 262
 QY 241 QSGRKADIMYGTVDQWRKIFRDEGGRAPFGKAMSVLRGMGAFLVLYDEIK 295
 DB 263 TSGEA--VKYSSFECCGRLAKKAGAPFGKAGANTLRGVAAGVLSYDQV 314

Search completed: December 18, 2003, 12:41:25
 Job time : 9.34267 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:34:56 ; Search time 35.2542 Seconds
(without alignments)
1337.197 Million cell updates/sec

Title: US-09-811-131-31

Perfect score: 1553

Sequence: 1 MGHANFLDPLAGAVAA.....LRGNGAFVLVDIKKV 297

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

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2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*

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23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1553	100.0	297	21	AAV71031
2	1553	100.0	297	22	AAU01198
3	1553	100.0	297	23	AAU01378
4	1457.5	93.9	298	19	AAU01169
5	1442.5	92.9	293	22	ABU53219
6	1398.5	90.1	298	23	AAO18516
7	1391.5	89.6	298	21	AAV71032
8	1391.5	89.6	298	22	AAU01199
9	1391.5	89.6	298	23	AAU01379

10	1385.5	89.2	298	21	AAV71033	Human adenine nucl
11	1385.5	89.2	298	22	AAU39641	Human polypeptide
12	1385.5	89.2	298	22	AAU01200	Human adenine nucl
13	1385.5	89.2	298	22	AAU01380	Human adenine nucl
14	1385.5	89.2	323	22	AAU41427	Human polypeptide
15	1294.5	83.4	325	22	ABG15423	Novel human diagne
16	1268.5	81.7	429	24	ABR41715	Human DTHP organe
17	1241	79.9	299	22	ABR66082	Drosophila melanog
18	1241	79.9	299	22	ABR67200	Drosophila melanog
19	1221.5	78.7	263	22	ABR67056	Novel human diagne
20	1147	73.9	307	22	ABR58380	Drosophila melanog
21	1101.5	70.9	315	22	ABU53218	Human metabolism-a
22	1101.5	70.9	315	23	AAK21175	Human TRICH-19 pro
23	926.5	59.7	228	23	ABP43205	Human ovarian anti
24	867.5	55.9	222	23	ABP74106	Human TRICH SEQ ID
25	820	52.8	298	22	ABG18922	Novel human diagne
26	771	49.6	301	23	ABP73357	Candida albicans e
27	746.5	48.1	379	24	ABP81267	Arabidopsis thalia
28	746	48.0	346	21	AAK36577	Arabidopsis thalia
29	746	48.0	346	21	AAK37261	Arabidopsis thalia
30	746	48.0	346	21	AAK37264	Arabidopsis thalia
31	746	48.0	346	21	AAK38460	Arabidopsis thalia
32	746	48.0	363	21	AAK36576	Arabidopsis thalia
33	746	48.0	363	21	AAK37260	Arabidopsis thalia
34	746	48.0	363	21	AAK37263	Arabidopsis thalia
35	746	48.0	363	21	AAK38459	Arabidopsis thalia
36	746	48.0	381	21	AAK36575	Arabidopsis thalia
37	746	48.0	381	21	AAK37259	Arabidopsis thalia
38	746	48.0	381	21	AAK37262	Arabidopsis thalia
39	746	48.0	381	21	AAK38458	Arabidopsis thalia
40	746	48.0	992	21	AAK38672	Arabidopsis thalia
41	746	48.0	1009	21	AAK38671	Arabidopsis thalia
42	746	48.0	1027	21	AAK38670	Arabidopsis thalia
43	743	47.8	346	21	AAK17731	Arabidopsis thalia
44	743	47.8	363	21	AAK17730	Arabidopsis thalia
45	743	47.8	381	21	AAK17729	Arabidopsis thalia

ALIGNMENTS

RESULT 1	AAV71031	standard; Protein; 297 AA.
ID	AAV71031	
AC	AAV71031	
XX		
DT	29-AUG-2000	(first entry)
XX		
DE	Human adenine nucleotide translocator ANTL.	
XX		
KW	Human; adenine nucleotide translocator; ANTL; mitochondria; ADP; ATP;	
KW	adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;	
KW	mitochondrial permeability transition; neuroprotective; noctropic;	
KW	antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;	
KW	antiparkinsonic; cerebroprotective; therapeutic; screening; psoriasis;	
KW	Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;	
KW	diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;	
KW	mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;	
KW	mitochondrial diabetes and deafness; hyperproliferative disorder;	
KW	myoclonic epilepsy red ragged fibre syndrome.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200026370-A2.	
XX		
PD	11-MAY-2000.	
XX		
PF	03-NOV-1999;	99WO-US25883.
XX		
PR	03-NOV-1998;	98US-0185904.
PR	08-SEP-1999;	99US-0393441.
XX		

PA (MITO-) MITOKOR.
 XX
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR,
 PI Ghosh SS;
 XX
 DR WPI, 2000-365619/31.
 DR N-PSDB; AAD00519.
 XX
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 XX
 PS Claim 44, Page 172, 175pp; English.
 XX
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT1 from human brain.
 XX
 SQ Sequence 297 AA;
 Query Match 100.0%; Score 1553; DB 21; Length 297;
 Best Local Similarity 100.0%; Pred. No. 3.4e-173;
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIEVKLLQVQHASKOISAEKQYKGIIDCVR 60
 DB 1 MGDHMSFLKDFLAGAANAASKTAVAPIEVKLLQVQHASKOISAEKQYKGIIDCVR 60
 QY 61 IPKEQGLSPFRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKGPMRYFAGNLASG 120
 DB 61 IPKEQGLSPFRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKGPMRYFAGNLASG 120
 QY 121 GAAGATSLCFYPLDFAFTRLAADVGRRAQREFFGLDPCIIKIKPSDGLRGLYGFNVSV 180
 DB 121 GAAGATSLCFYPLDFAFTRLAADVGRRAQREFFGLDPCIIKIKPSDGLRGLYGFNVSV 180
 QY 181 QGIIYRAAYGVYDTAKGMLPDPKNVHIFVSMIAOSVAVAGLSYFPDTRRRMMQ 240
 DB 181 QGIIYRAAYGVYDTAKGMLPDPKNVHIFVSMIAOSVAVAGLSYFPDTRRRMMQ 240
 QY 241 SGRKADIMYGTVDCKRKIADEGAKAFKGAWSNVLKMGGAFLVLYDEIKKYV 297
 DB 241 SGRKADIMYGTVDCKRKIADEGAKAFKGAWSNVLKMGGAFLVLYDEIKKYV 297

RESULT 2
 AAU01198
 ID AAU01198 standard; Protein; 297 AA.
 AC AAU01198;
 XX
 XX 07-SEP-2001 (first entry)
 DT
 XX
 DE Human adenine nucleotide translocator-1 (ANT-1) protein.
 XX
 XX Human; adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

XX
 OS Homo sapiens.
 XX
 PN WO200132876-A2.
 XX
 PD 10-MAY-2001.
 XX
 PF 03-NOV-2000; 2000WO-US30535.
 XX
 PR 03-NOV-1999; 99US-0434354.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Fritger LG;
 PI Veljiceleb G, Davis RE;
 XX
 DR WPI, 2001-291054/30.
 DR N-PSDB; AAS05901.
 XX
 PS New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX
 PS Disclosure; Fig 2; 186pp; English.
 XX
 CC The present sequence represents human adenine nucleotide translocator-1
 CC (ANT-1) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLAISH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 XX
 SQ Sequence 297 AA;
 Query Match 100.0%; Score 1553; DB 22; Length 297;
 Best Local Similarity 100.0%; Pred. No. 3.4e-173;
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIEVKLLQVQHASKOISAEKQYKGIIDCVR 60
 DB 1 MGDHMSFLKDFLAGAANAASKTAVAPIEVKLLQVQHASKOISAEKQYKGIIDCVR 60
 QY 61 IPKEQGLSPFRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKGPMRYFAGNLASG 120
 DB 61 IPKEQGLSPFRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKGPMRYFAGNLASG 120
 QY 121 GAAGATSLCFYPLDFAFTRLAADVGRRAQREFFGLDPCIIKIKPSDGLRGLYGFNVSV 180
 DB 121 GAAGATSLCFYPLDFAFTRLAADVGRRAQREFFGLDPCIIKIKPSDGLRGLYGFNVSV 180
 QY 181 QGIIYRAAYGVYDTAKGMLPDPKNVHIFVSMIAOSVAVAGLSYFPDTRRRMMQ 240
 DB 181 QGIIYRAAYGVYDTAKGMLPDPKNVHIFVSMIAOSVAVAGLSYFPDTRRRMMQ 240
 QY 241 SGRKADIMYGTVDCKRKIADEGAKAFKGAWSNVLKMGGAFLVLYDEIKKYV 297
 DB 241 SGRKADIMYGTVDCKRKIADEGAKAFKGAWSNVLKMGGAFLVLYDEIKKYV 297

RESULT 3
AAU10378
ID AAU10378 standard; Protein; 297 AA.
XX
AC AAU10378;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human adenine nucleotide translocator 1 (ANT1).
XX
KW Human; adenine nucleotide translocator; ANT;
KM mitochondrial matrix protein.
XX
OS Homo sapiens.
XX
PN MO200185944-A2.
PD 15-NOV-2001.
XX
PF 11-MAY-2001; 2001WO-US15416.
XX
PR 11-MAY-2000; 2000US-0569327.
XX
PA (MITO-) MITOKOR.
XX
PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;
PI Ghosh SS, Moos WH, Felt Y, Carroll AK;
XX
DR WPI; 2002-055598/07.
DR N-PSDB; AAS16688.
XX
XX
PT Novel recombinant expression construct for producing adenine nucleotide
PT translocator polypeptides, comprises a regulated promoter linked to
PT nucleic acid encoding the polypeptide
XX
PS Claim 44; Fig 2; 147p; English.
XX
CC The invention relates to a recombinant expression construct (I)
CC comprising a regulated promoter operably linked to a nucleic acid
CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
CC proteins mediate the exchange of ATP synthesized in the mitochondrial
CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
CC culturing the host cell. (I) is also useful for targeting a polypeptide
CC of interest to a mitochondrial membrane, where ANT polypeptide is
CC expressed as a fusion protein with the polypeptide of interest.
CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
CC useful for identifying an agent that binds to an ANT polypeptide. ANT
CC ligand is useful for determining the presence of an ANT polypeptide.
CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
CC ANT from a biological sample, where the ANT ligand is covalently or non-
CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
CC useful for identifying an agent that interacts with an ANT polypeptide.
CC The present sequence represents the amino acid sequence of human ANT1.
XX
SQ Sequence 297 AA;
Query Match 100.0%; Score 1553; DB 23; Length 297;
Best Local Similarity 100.0%; Pred. No. 3.4e-173;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

181 QGIIYRAAYGVYDTAKGMLPDKVNHIFVSMWIAQSVTAVALSLSPEDTVRRMMQ 240
181 QGIIYRAAYGVYDTAKGMLPDKVNHIFVSMWIAQSVTAVALSLSPEDTVRRMMQ 240
241 SGRKADIMYTGTVDCWRKIAKDEGAFKGAWSNVLKMGAFVLVLYDEIKKYV 297
241 SGRKADIMYTGTVDCWRKIAKDEGAFKGAWSNVLKMGAFVLVLYDEIKKYV 297
RESULT 4
AAW61169
ID AAW61169 standard; Protein; 298 AA.
XX
AC AAW61169;
XX
DT 28-SEP-1998 (first entry)
XX
DE Ant1 protein.
XX
KW Ant1; Adenine nucleotide translocator; cloning; screening;
KW DNA Tag dideoxy terminator cycle sequencing; oxidative phosphorylation;
KW probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy;
KW hypertrophic cardiomyopathy; fasciocalcular humeral muscular dystrophy;
KW lactic acidosis; degenerative muscle disease.
XX
OS Mus sp.
XX
PN WO9819714-A1.
XX
PD 14-MAY-1998.
XX
PF 31-OCT-1997; 97WO-US19882.
XX
PR 01-NOV-1996; 96US-0030017.
XX
PA (UYEM-) UNIV EMORY.
XX
PI Graham BC, Macgregor GR, Wallace DC;
XX
DR WPI; 1998-286608/25.
DR N-PSDB; AAV36479.
XX
XX
PT Mice lacking heart-muscle adenine nucleotide translocator protein -
PT useful as model for mitochondrial myopathy and hypertrophic
PT cardiomyopathy in animals and to test therapeutic compositions or
PT gene therapies
XX
PS Disclosure; Page 39-40; 61p; English.
XX
CC The present sequence is the mouse Ant1 protein, the cDNA producing this
CC polypeptide is cloned by screening a mouse heart cDNA library with the
CC human Ant1 cDNA as a probe. The Ant1 cDNA sequence was determined by DNA
CC Tag dideoxy terminator cycle sequencing. The Ant1 protein is encoded by
CC the Ant1 locus, a nuclear gene on chromosome 8. This protein is required
CC in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP
CC which can then be converted into ATP. An Ant1 homozygous mutant would
CC thus be defective in OXPHOS which results in disease in oxidative
CC metabolism dependent tissues. This mouse Ant1 homozygous mutant can be
CC used as a model system for fasciocalcular humeral muscular dystrophy,
CC hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model
CC systems can be used to test possible therapeutic compounds which
CC increase/mediate ATP and ADP exchange across the mitochondrial membrane
CC independent of ANT1.
XX
SQ Sequence 298 AA;
Query Match 93.9%; Score 1457.5; DB 19; Length 298;
Best Local Similarity 93.6%; Pred. No. 5.4e-162;
Matches 279; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

QY 61 IPEKGLSPKRNGLNANVIRYPTALNPAFKDKTKOLFLGSDVDRHKQFWRYPAGNLASG 120
 DB 61 IPEKGLSPKRNGLNANVIRYPTALNPAFKDKTKOLFLGSDVDRHKQFWRYPAGNLASG 120
 QY 121 GAAGTSLCPYVPLDPAFTRTLADVGR-RAOREFPLGDBCIIRKPSDGLRGLYOGFNVSGI 179
 DB 121 GAAGTSLCPYVPLDPAFTRTLADVGR-RAOREFPLGDBCIIRKPSDGLRGLYOGFNVSGI 180
 QY 180 VOGIIIVRAAYFGVYDTAKGMLPDPKXVHIIVSWMIASQSVTAVALGLSYPPDTRRRMM 239
 DB 181 VOGIIIVRAAYFGVYDTAKGMLPDPKXVHIIVSWMIASQSVTAVALGLSYPPDTRRRMM 240
 QY 240 QSGRRGADIMYTGTDCKRKLAKDEGAKAFPKGANSNVLRGGAFVLVLYDEIKKY 297
 DB 241 QSGRRGADIMYTGTDCKRKLAKDEGAKAFPKGANSNVLRGGAFVLVLYDEIKKY 298

RESULT 5

ABUS3219
 ID ABUS3219 standard; Protein; 293 AA.

AC ABUS3219;
 DT 14-APR-2003 (first entry)
 DE Human metabolism-associated DKFZphtest3_35n12 homologue #1.
 KW Human; gene therapy; vaccine; disease treatment; detection.
 OS Homo sapiens.
 PN WO200112659-A2.
 PD 22-FEB-2001.
 PF 18-AUG-2000; 2000WO-1B01496.
 PR 18-AUG-1999; 99US-0149499.
 PR 28-SEP-1999; 99US-0156503.
 XX (GERTU-) GERMAN HUMAN GENOME PROJECT.
 PA Wiemann S;
 PI WPI; 2001-327840/34.
 PT Nucleic acids having the sequences of clones isolated from libraries of
 PT different human tissues, useful in recombinant DNA methodologies -
 XX Example III; Page 850; 1095pp; English.
 CC This invention describes novel polynucleotides and polypeptides isolated
 CC from human cDNA libraries which can be used for gene therapy or in
 CC vaccines. The polynucleotides of the invention and antibodies encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate polypeptide expression. The products of the
 CC invention may also be used to identify modulators of expression and
 CC activity and to down regulate expression and activity. The antibodies of
 CC the invention may also be used as diagnostic agents for detecting the
 CC presence of polypeptides in samples. This sequence represents a homologue
 CC of a polypeptide described in the disclosure of the invention.

Sequence 293 AA;

Query Match 92.9%; Score 1442.5; DB 22; Length 293;
 Best Local Similarity 94.2%; Pred. No. 3e-160;
 Matches 276; Conservative 10; Mismatches 6; Indels 1; Gaps 1;

QY 5 AMSFLKDFLAGAANAASVTAAVAFIERVTLLOVOHASQVIAEKQYKGIIDCVRIPE 64
 DB 1 ALSFLKDFLAGAANAASVTAAVAFIERVTLLOVOHASQVIAEKQYKGIIDCVRIPE 60

QY 65 QGFLSPKRNGLNANVIRYPTALNPAFKDKTKOLFLGSDVDRHKQFWRYPAGNLASGAG 124
 DB 61 QGFLSPKRNGLNANVIRYPTALNPAFKDKTKOLFLGSDVDRHKQFWRYPAGNLASGAG 120
 QY 125 ATSLCFYVPLDPAFTRTLADVGR-RAOREFPLGDBCIIRKPSDGLRGLYOGFNVSGI 183
 DB 121 ATSLCFYVPLDPAFTRTLADVGR-RAOREFPLGDBCIIRKPSDGLRGLYOGFNVSGI 180
 QY 184 IIVRAAYFGVYDTAKGMLPDPKXVHIIVSWMIASQSVTAVALGLSYPPDTRRRMM 243
 DB 181 IIVRAAYFGVYDTAKGMLPDPKXVHIIVSWMIASQSVTAVALGLSYPPDTRRRMM 240
 QY 244 KGADIMYTGTDCKRKLAKDEGAKAFPKGANSNVLRGGAFVLVLYDEIKKY 296
 DB 241 KGADIMYTGTDCKRKLAKDEGAKAFPKGANSNVLRGGAFVLVLYDEIKKY 293

RESULT 6

AAO18516
 ID AAO18516 standard; Protein; 298 AA.

AC AAO18516;
 DT 11-OCT-2002 (first entry)
 DE Human insulin receptor signaling modifier SEQ ID NO: 54.
 KW Human; insulin receptor signaling; insulin receptor signaling modifier;
 KW ISM; diabetes; metabolic syndrome; antidiabetic.

OS Homo sapiens.

PN WO200255664-A2.

PD 18-JUL-2002.

PF 11-JAN-2002; 2002WO-US01048.

PR 12-JAN-2001; 2001US-261226P.
 PR 12-JAN-2001; 2001US-261303P.
 PR 12-JAN-2001; 2001US-261304P.
 PR 12-JAN-2001; 2001US-261335P.
 PR 12-JAN-2001; 2001US-261361P.
 PR 12-JAN-2001; 2001US-261361P.
 PR 12-JAN-2001; 2001US-261456P.
 PR 12-JAN-2001; 2001US-261457P.
 PR 12-JAN-2001; 2001US-261458P.
 PR 12-JAN-2001; 2001US-261459P.
 PR 12-JAN-2001; 2001US-261461P.
 PR 12-JAN-2001; 2001US-261518P.
 PR 12-JAN-2001; 2001US-261531P.
 PR 12-JAN-2001; 2001US-261532P.
 PR 12-JAN-2001; 2001US-261589P.
 PR 12-JAN-2001; 2001US-261590P.
 PR 12-JAN-2001; 2001US-261694P.
 PR 12-JAN-2001; 2001US-261695P.
 PR 12-JAN-2001; 2001US-261697P.

PA (EXEL-) EXELIXIS INC.

PI Seidel-Dugan C, Ferguson KC, Kidd T;

DR WPI; 2002-599664/64.

DR N-PSDB; AAL48635.

PT Identifying an insulin receptor signaling modulator, useful as drug
 PT targets for treating diabetes or metabolic disorders, comprises
 PT contacting an assay system comprising insulin receptor signaling
 PT modifiers with a test agent -

Disclousure; Page 160-161; 232pp; English.

The present invention relates to a method of identifying a candidate

CC insulin receptor (INR) signaling modulating agent, involving contacting
CC an assay system comprising an insulin receptor signaling modifier (ISM)
CC polypeptide or nucleic acid with a test agent, and detecting a test
CC agent-biased activity of the assay system. The method is useful for
CC identifying candidate INR signaling modulating agents. ISM genes may be
CC used as drug targets for treatment of disorders related to INR signaling
CC such as diabetes or metabolic syndrome. ISM nucleic acids and
CC polypeptides are useful for identifying and testing agents that modulate
CC ISM function and for other applications related to the involvement of ISM
CC in INR signaling, and for identifying subjects having a predisposition to
CC such diseases associated with INR signaling. The present sequence is an
CC ISM protein described in the exemplification of the invention.

XX Sequence 298 AA;

Query Match 90.1%; Score 1398.5; DB 23; Length 298;
Best Local Similarity 88.9%; Pred. No. 4.5e-155;
Matches 264; Conservative 17; Mismatches 15; Indels 1; Gaps 1;

QY 1 MGDHMSPLDPLAGVAAVSKTAVAPIERVKLLDVOHASKOISAEKQYGIIDCVR 60
DB 1 MTDAAVSFADPLAGVAAVSKTAVAPIERVKLLDVOHASKOITADKQYGIIDCVR 60
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDVRHQPFRYFAGNLASG 120
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDVRHQPFRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDPAFRTLADVGR-AQREHFGIDCIIKIFKSDGLRGLYQGFNV 179
DB 121 GAAGATSLCFVYPLDPAFRTLADVGR-AQREHFGIDCIIKIFKSDGLRGLYQGFNV 180
QY 180 VQGIITIRAAVFGYVDPKAKMLDPPKVNHFVSMWIAOSTYAVAGLSYPPDYRRMM 239
DB 181 VQGIITIRAAVFGYVDPKAKMLDPPKVNHFVSMWIAOSTYAVAGLSYPPDYRRMM 240
QY 240 QSGRKGADIMYTGVDCKRIKADGAKAFPGKAMSVNLGSGAFVLYYDEIKKY 296
DB 241 QSGRKGADIMYTGVDCKRIKADGAKAFPGKAMSVNLGSGAFVLYYDEIKKY 297

RESULT 7
AAV71032
ID AAV71032 standard; Protein; 298 AA.

XX AAV71032;

XX 29-AUG-2000 (first entry)

DE Human adenine nucleotide translocator ANT2.

XX Human, adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP;
KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
KW mitochondrial permeability transition; neuroprotective; nocrotic;
KW antiParkinsonian; cytoleptic; antidiabetic; anticonvulsant; neuroleptic;
KW antipsychotic; cerebroprotective; therapeutic; screening; psoriasis;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
KW mitochondrial diabetes and deafness; hyperproliferative disorder;
KW myoclonic epilepsy red ragged fibre syndrome.

XX Homo sapiens.

OS WO200026370-A2.

XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-US25883.

XX 03-NOV-1998; 98US-0185904.

XX 08-SEP-1999; 99US-0333441.

XX (MITO-) MITOKOR.

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
PI Ghosh SS;
XX WPI; 2000-365619/31.
DR N-PSDB; AAD00520.
XX Recombinant construct encoding adenine nucleotide translocator
PT polypeptide, useful e.g. in screening for potential therapeutic agents
PT against mitochondrial disease
XX Claim 45; Page 172-173; 175pp; English.

CC The patent discloses a method to produce adenine nucleotide translocator
CC (ANT) proteins or ANT fusion proteins using recombinant expression
CC constructs. ANT is a nuclear encoded protein and a major component of
CC inner mitochondrial membrane. It mediates transport of adenosine
CC di/tri-phosphates across the mitochondrial inner membrane and also serves
CC as an important molecular component of the mitochondrial permeability
CC transition pore, a modulator of apoptosis. ANT is used to identify agents
CC or ligands that bind to, or interact with it. The ANT ligands are used to
CC detect or isolate ANT in a biological sample, and therapeutically for
CC regulating mitochondrial pore activity, for treating diseases associated
CC with altered mitochondrial function, including Alzheimer's, Parkinson's
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondria
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
CC epilepsy red ragged fibre syndrome. The present sequence is an
CC adenine nucleotide translocator ANT2 from human brain.

XX Sequence 298 AA;

Query Match 89.6%; Score 1391.5; DB 21; Length 298;
Best Local Similarity 88.6%; Pred. No. 3e-154;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSPLDPLAGVAAVSKTAVAPIERVKLLDVOHASKOISAEKQYGIIDCVR 60
DB 1 MTDAAVSFADPLAGVAAVSKTAVAPIERVKLLDVOHASKOITADKQYGIIDCVR 60
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDVRHQPFRYFAGNLASG 120
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDVRHQPFRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDPAFRTLADVGR-AQREHFGIDCIIKIFKSDGLRGLYQGFNV 179
DB 121 GAAGATSLCFVYPLDPAFRTLADVGR-AQREHFGIDCIIKIFKSDGLRGLYQGFNV 180
QY 180 VQGIITIRAAVFGYVDPKAKMLDPPKVNHFVSMWIAOSTYAVAGLSYPPDYRRMM 239
DB 181 VQGIITIRAAVFGYVDPKAKMLDPPKVNHFVSMWIAOSTYAVAGLSYPPDYRRMM 240
QY 240 QSGRKGADIMYTGVDCKRIKADGAKAFPGKAMSVNLGSGAFVLYYDEIKKY 296
DB 241 QSGRKGADIMYTGVDCKRIKADGAKAFPGKAMSVNLGSGAFVLYYDEIKKY 297

RESULT 8
AAU01199
ID AAU01199 standard; Protein; 298 AA.

XX AAU01199;

XX 07-SEP-2001 (first entry)

DE Human adenine nucleotide translocator-2 (ANT-2) protein.

XX Human, adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;
KW mitochondrial permeability transition pore component; cell survival;
KW mitochondrial core component; mitochondrial related disorder; cancer;
KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

OS Homo sapiens.
 XX WO200132876-A2.
 XX 10-MAY-2001.
 PD 03-NOV-2000; 2000WO-US30535.
 XX 03-NOV-1999; 99US-0434354.
 PR (MITO-) MITOKOR.
 XX Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigert LG;
 PI Veliceteb G, Davis RE;
 XX WPI; 2001-291054/30.
 DR N-PSDB; AAS05902.
 PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX
 PS Disclosure; Fig 2; 186pp; English.
 CC The present sequence represents human adenine nucleotide translocator-2
 CC (ANT-2) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASh sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 CC
 SQ Sequence 298 AA;
 Query Match 89.6%; Score 1391.5; DB 22; Length 298;
 Best Local Similarity 88.6%; Pred. No. 3e-154;
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIRVYKLLQVQHSKQISAEKQYGIIDCVVR 60
 DB 1 MTDALSPAKDFLAGAANAASKTAVAPIRVYKLLQVQHSKQITADKQYGIIDCVVR 60
 QY 61 IPKEQGFSPFRGNLANVIRFPFOALNFAFKDKYKQFLGVDNRHKKQFWRYPAGNLASG 120
 DB 61 IPKEQGVLSFPRGNLANVIRFPFOALNFAFKDKYKQIFLGVDNRTOFWRYPAGNLASG 120
 QY 121 GAAGATSLCFYYPIDLPARTRLAADVGRR-AORBEFHGLDCCIIRKPSGDLGLYOGGFNV 179
 DB 121 GAAGATSLCFYYPIDLPARTRLAADVGRR-AORBEFHGLDCCIIRKPSGDLGLYOGGFNV 180
 QY 180 VQGIITRAAYFGVYDTRAKMLPDPKXVHIFVSNMIAOSVTAAGLSTYPPDYRRRRMM 239
 DB 181 VQGIITRAAYFGVYDTRAKMLPDPKXVHIFVSNMIAOTVTAAGLSTYPPDYRRRRMM 240
 QY 240 QSGRKGADIMTGTVDCKRKLANDEGAFAFFKGAANSVLRGKGAFTVLVDIEIKKY 296
 DB 241 QSGRKGADIMTGTVDCKRKLANDEGAFAFFKGAANSVLRGKGAFTVLVDIEIKKY 297

RESULT 9

AAU10379
 ID AAU10379 standard; Protein; 298 AA.
 XX
 AC AAU10379;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Human adenine nucleotide translocator 2 (ANT2).
 XX
 KW Human; adenine nucleotide translocator; ANT; ss;
 KW mitochondrial matrix protein.
 XX
 OS Homo sapiens.
 XX WO200185944-A2.
 XX 15-NOV-2001.
 PD 11-MAY-2001; 2001WO-US15416.
 XX
 PR 11-MAY-2000; 2000US-0569327.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS, Moos WH, Pei Y, Carroll AK;
 XX WPI; 2002-055598/07.
 DR N-PSDB; AAS16689.
 PT Novel recombinant expression construct for producing adenine nucleotide
 PT translocator polypeptides, comprises a regulated promoter linked to
 PT nucleic acid encoding the polypeptide -
 XX
 PS Claim 44; Fig 2; 147pp; English.
 CC The invention relates to a recombinant expression construct (I)
 CC comprising a regulated promoter operably linked to a nucleic acid
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
 CC culturing the host cell. (I) is also useful for targeting a polypeptide
 CC of interest to a mitochondrial membrane, where ANT polypeptide is
 CC expressed as a fusion protein with the polypeptide of interest.
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT
 CC ligand is useful for determining the presence of an ANT polypeptide,
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
 CC ANT from a biological sample, where the ANT ligand is covalently or non-
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
 CC useful for identifying an agent that interacts with an ANT polypeptide.
 CC The present sequence represents the amino acid sequence of human ANT2.
 CC
 SQ Sequence 298 AA;
 Query Match 89.6%; Score 1391.5; DB 23; Length 298;
 Best Local Similarity 88.6%; Pred. No. 3e-154;
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIRVYKLLQVQHSKQISAEKQYGIIDCVVR 60
 DB 1 MTDALSPAKDFLAGAANAASKTAVAPIRVYKLLQVQHSKQITADKQYGIIDCVVR 60
 QY 61 IPKEQGFSPFRGNLANVIRFPFOALNFAFKDKYKQFLGVDNRHKKQFWRYPAGNLASG 120
 DB 61 IPKEQGVLSFPRGNLANVIRFPFOALNFAFKDKYKQIFLGVDNRTOFWRYPAGNLASG 120
 QY 121 GAAGATSLCFYYPIDLPARTRLAADVGRR-AORBEFHGLDCCIIRKPSGDLGLYOGGFNV 179
 DB 121 GAAGATSLCFYYPIDLPARTRLAADVGRR-AORBEFHGLDCCIIRKPSGDLGLYOGGFNV 180
 QY 180 VQGIITRAAYFGVYDTRAKMLPDPKXVHIFVSNMIAOSVTAAGLSTYPPDYRRRRMM 239

Db 181 VGGIIRAAVFGYIDFAKGLPDPKXTHIVISWMIAGTVAVAGLTSYPTDTRRRMM 240
 QY 240 QSGRKGADIMVTGVDGCRKRIADGGAAPFKGAMSVNLRGMGAFVLVYDEIKKY 296
 Db 241 QSGRKGADIMVTGTLDCWRKLIARDEGGAFPKGAMSVNLRGMGAFVLVYDEIKKY 297

RESULT 10
 ID AAY71033 standard; Protein, 298 AA.
 AC AAY71033;
 XX 29-AUG-2000 (first entry)
 DE Human adenine nucleotide translocator ANT3.
 XX Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;
 KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
 KW mitochondrial permeability transition; neuroprotective; neurotropic;
 KW antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
 KW antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
 KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
 KW mitochondrial encephalopathy; lactic acidosis; stroke; MTD;
 KW mitochondrial diabetes and deafness; hyperproliferative disorder;
 KW myoclonic epilepsy red ragged fibre syndrome.
 XX Homo sapiens.
 OS WO200026370-A2.
 XX 11-MAY-2000.
 XX 03-NOV-1999; 99WO-US25883.
 XX 03-NOV-1998; 98US-0185904.
 PR 08-SEP-1999; 99US-0393441.
 XX (MITO-) MITOKOR.
 PA Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR,
 PI Ghosh SS;
 DR WPI; 2000-365619/31.
 DR N-PSDB; AAD00521.
 XX Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 PS Claim 46; Page 173-174; 175pp; English.
 XX The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression of
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MTD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT3 from human brain.
 XX Sequence 298 AA;
 XX SQ

Query Match 89.2%; Score 1385.5; DB 21; Length 298;
 Best Local Similarity 87.2%; Pred. No. 1.5e-153;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHWSFLKDFLAGAANAASKTAVAPISRVKLLQVONASKOISAEKOYKGIIDCVR 60
 Db 1 MTEGALISFADDFLAGGIAAASKTAVAPISRVKLLQVONASKOIADKQKGVDCIVR 60
 QY 61 IPKQGFSLFMRGNLANVIRFPQALNPAFKDKYKQLFUGGVDRHKQFMRYPAGNLSG 120
 Db 61 IPKQGFSLFMRGNLANVIRFPQALNPAFKDKYKQLFUGGVDRHKQFMRYPAGNLSG 120
 QY 121 GAAGATSLCFVYPLDFAFRTLADVGR-AGREHGGDCLIKFKSDGRLGYOGFNV 179
 Db 121 GAAGATSLCFVYPLDFAFRTLADVGR-AGREHGGDCLIKFKSDGRLGYOGFNV 180
 QY 180 VGGIIRAAVFGYIDFAKGLPDPKXTHIVISWMIAGTVAVAGLTSYPTDTRRRMM 239
 Db 181 VGGIIRAAVFGYIDFAKGLPDPKXTHIVISWMIAGTVAVAGLTSYPTDTRRRMM 240
 QY 240 QSGRKGADIMVTGVDGCRKRIADGGAAPFKGAMSVNLRGMGAFVLVYDEIKKY 297
 Db 241 QSGRKGADIMVTGVDGCRKRIADGGAAPFKGAMSVNLRGMGAFVLVYDEIKKY 298

RESULT 11
 ID AAM39641 standard; Protein, 298 AA.
 AC AAM39641;
 XX 22-OCT-2001 (first entry)
 DE Human polypeptide SEQ ID NO 2786.
 XX Human; neurotropic; immunosuppressant; cytosolic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX Homo sapiens.
 OS WO200153312-A1.
 XX 26-JUL-2001.
 XX 26-DEC-2000; 2000WO-US34263.
 XX 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX (HYSR-) HYSRQ INC.
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 DR WPI; 2001-442253/47.
 DR N-PSDB; AA158797.
 XX Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX Example 4; SEQ ID NO 2786; 10078bp; English.
 XX PS

XX The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM3642-AAM42213) with nootropic,
 CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localized neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilization of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.

XX Sequence 298 AA;

Query Match 89.2%; Score 1385.5; DB 22; Length 298;

Best Local Similarity 87.2%; Pred. No. 1.5e-153; Mismatches 16; Indels 1; Gaps 1;

Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCYR 60
 DB 1 MTEQALISPAKDFLAGIAAIAISKTAAPIERVKLLQVQHASKOIAADKQYKGIIDCYR 60
 QY 1 PKKQGLSPFRGNLANVIRFPYQALNPAFKDKYKOLFLGGVDHKKQFMRFPAGNLASG 120
 DB 1 PKKQGLSPFRGNLANVIRFPYQALNPAFKDKYKOLFLGGVDHKKQFMRFPAGNLASG 120
 QY 121 GAAGATSLCFYYPDPAFTRLAADVGR-AQREPHGLDCCIIFKSDGLRGLYOGFNVS 179
 DB 121 GAAGATSLCFYYPDPAFTRLAADVGR-AQREPHGLDCCIIFKSDGLRGLYOGFNVS 180
 QY 180 VGGIITVRAAYFGVYDTAKGMLPDPKKNHIFVSMWIAQSVTAVALLSYPPDYRRMM 239
 DB 180 VGGIITVRAAYFGVYDTAKGMLPDPKKNHIFVSMWIAQSVTAVALLSYPPDYRRMM 240
 QY 240 QSGRKGADIMYTGVDCKRKIADEGAKAFPKGAMSVNLKMGAFVLYLDELKVI 297
 DB 241 QSGRKGADIMYTGVDCKRKIFRDEGKAFFPKGAMSVNLKMGAFVLYLDELKVI 298

RESULT 12

AAU01200 standard; Protein; 298 AA.

AAU01200;

07-SEP-2001 (first entry)

Human adenine nucleotide translocator-3 (ANT-3) protein.

Human, adenine nucleotide translocator-3; ANT-3; MTP, cyclophilin;
 mitochondrial permeability transition pore component; cell survival;
 mitochondrial core component; mitochondrial related disorder; cancer;
 Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

Homo sapiens.

MO200132876-A2.

10-MAY-2001.

03-NOV-2000; 2000WO-US30535.

03-NOV-1999; 99US-0434354.

(MITO-) MITOKOR.

Murphy AN, Cleverger W, Wiley SE, Andreyev AY, Frigeri LG;

PI Velicelaeb1 G, Davis RE;

DR WPI; 2001-291054/30.

DR N-PSDB; AAS05903.

PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -

PS Disclosure; Fig 2; 186pp; English.

XX The present sequence represents human adenine nucleotide translocator-3
 CC (ANT-3) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLAHS sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.

XX Sequence 298 AA;

Query Match 89.2%; Score 1385.5; DB 22; Length 298;

Best Local Similarity 87.2%; Pred. No. 1.5e-153; Mismatches 16; Indels 1; Gaps 1;

Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCYR 60
 DB 1 MTEQALISPAKDFLAGIAAIAISKTAAPIERVKLLQVQHASKOIAADKQYKGIIDCYR 60
 QY 1 PKKQGLSPFRGNLANVIRFPYQALNPAFKDKYKOLFLGGVDHKKQFMRFPAGNLASG 120
 DB 1 PKKQGLSPFRGNLANVIRFPYQALNPAFKDKYKOLFLGGVDHKKQFMRFPAGNLASG 120
 QY 61 IPKQGLSPFRGNLANVIRFPYQALNPAFKDKYKOLFLGGVDHKKQFMRFPAGNLASG 120
 DB 61 IPKQGLSPFRGNLANVIRFPYQALNPAFKDKYKOLFLGGVDHKKQFMRFPAGNLASG 120
 QY 121 GAAGATSLCFYYPDPAFTRLAADVGR-AQREPHGLDCCIIFKSDGLRGLYOGFNVS 179
 DB 121 GAAGATSLCFYYPDPAFTRLAADVGR-AQREPHGLDCCIIFKSDGLRGLYOGFNVS 180
 QY 180 VGGIITVRAAYFGVYDTAKGMLPDPKKNHIFVSMWIAQSVTAVALLSYPPDYRRMM 239
 DB 180 VGGIITVRAAYFGVYDTAKGMLPDPKKNHIFVSMWIAQSVTAVALLSYPPDYRRMM 240
 QY 240 QSGRKGADIMYTGVDCKRKIADEGAKAFPKGAMSVNLKMGAFVLYLDELKVI 297
 DB 241 QSGRKGADIMYTGVDCKRKIFRDEGKAFFPKGAMSVNLKMGAFVLYLDELKVI 298

RESULT 13

AAU10380 standard; Protein; 298 AA.

AAU10380;

14-FEB-2002 (first entry)

Human adenine nucleotide translocator 3 (ANT3).

Human, adenine nucleotide translocator; ANT;
 mitochondrial matrix protein.

Homo sapiens.

XX XX WO200185944-A2.
 XX FN
 XX PD 15-NOV-2001.
 XX PF 11-MAY-2001; 2001WO-US15416.
 XX PR 11-MAY-2000; 2000US-0556327.
 XX (MITO-) MITOKOR.
 XX PI Anderson CM, Davis RB, Clevenger W, Wiley SE, Miller SW, Szabo TR,
 XX PI Ghosh SS, Moos WH, Pei Y, Carroll AK,
 XX DR WPI: 2002-055598/07.
 XX N-PSDB; AAS16690.
 XX PT Novel recombinant expression construct for producing adenine nucleotide
 XX PT translocator polypeptides, comprises a regulated promoter linked to
 XX PT nucleic acid encoding the polypeptide -
 XX PS Example 3; Fig 2; 147pp; English.
 XX XX The invention relates to a recombinant expression construct (I)
 CC comprising a regulated promoter operably linked to a nucleic acid
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
 CC culturing the host cell. (I) is also useful for targeting a polypeptide
 CC of interest to a mitochondrial membrane, where ANT polypeptide is
 CC expressed as a fusion protein with the polypeptide of interest.
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT
 CC ligand is useful for determining the presence of an ANT polypeptide,
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
 CC ANT from a biological sample, where the ANT ligand is covalently or non-
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
 CC useful for identifying an agent that interacts with an ANT polypeptide.
 CC The present sequence represents the amino acid sequence of human ANT3.
 XX SQ Sequence 298 AA;
 Query Match 89.2%; Score 1385.5; DB 23; Length 298;
 Best Local Similarity 87.2%; Pred. No. 1.5e-153;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
 QY 1 MGDHWSFLKDFLAGAANAASKTAVAPIERVKLLQVQASKOISAEKQYKGIIDCVVR 60
 DB 1 MTEQALISAFKDFLAGGIAAISKTAIVAPIERVKLLQVQASKOIADKQKGIIDCVVR 60
 QY 61 IPKEQGLSPFRGNLANVIRYFPFOALNPAFKDKYKQIFLGVDVRHKOFRYFAGNLASG 120
 DB 61 IPKEQGLSPFRGNLANVIRYFPFOALNPAFKDKYKQIFLGVDVRHKOFRYFAGNLASG 120
 QY 121 GAAATSTSCFYVPLDPAFTRLAADVGR-AQREPHGIGDCTIKIFKSGKAGLYQGRNVS 179
 DB 121 GAAATSTSCFYVPLDPAFTRLAADVGR-AQREPHGIGDCTIKIFKSGKAGLYQGRNVS 180
 QY 180 VQGIITVRAAFYGVYDZAKGMLPDKNVHIFVSWMIAQSVTAVALGLSTPDTYRRMM 239
 DB 180 VQGIITVRAAFYGVYDZAKGMLPDKNVHIFVSWMIAQSVTAVALGLSTPDTYRRMM 240
 QY 240 QSGRKGADIMYTGVDICWRKIAKDEGAKAFPKGANSVNLKMGAFVVLVDEIKKYV 297
 DB 241 QSGRKGADIMYTGVDICWRKIFDEGKGAFFKGAANSVNLKMGAFVVLVDEIKKYV 298

XX XX 22-OCT-2001 (first entry)
 XX DT
 XX XX Human polypeptide SEQ ID NO 6358.
 XX DE
 XX KW Human; nootropic; immunosuppressant; cytoskeletal; gene therapy; cancer;
 XX KW peripheral nervous system; neuropathy; central nervous system; CNS;
 XX KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 XX KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 XX KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
 XX KW leukaemia.
 XX OS Homo sapiens.
 XX XX WO200153312-A1.
 XX PN 26-JUL-2001.
 XX PD 26-DEC-2000; 2000WO-US34263.
 XX PF 21-JAN-2000; 2000US-0488725.
 XX PR 25-APR-2000; 2000US-0552317.
 XX PR 09-JUL-2000; 2000US-0598042.
 XX PR 19-JUL-2000; 2000US-0620312.
 XX PR 03-AUG-2000; 2000US-0653450.
 XX PR 14-SEP-2000; 2000US-0662191.
 XX PR 19-OCT-2000; 2000US-0683036.
 XX PR 29-NOV-2000; 2000US-0727344.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 XX PI Wang J, Wang Z, Wehrman T, Xu C, Xue AD, Yang Y, Zhang J;
 XX PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX DR WPI: 2001-442253/47.
 XX DR N-PSDB; AAI60583.
 XX XX Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX PT
 XX PS Example 2; SEQ ID NO 6358; 10078pp; English.
 XX XX The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AA438642-AA442213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC activation/inhibition activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX SQ Sequence 323 AA;
 Query Match 89.2%; Score 1385.5; DB 22; Length 323;
 Best Local Similarity 87.2%; Pred. No. 1.7e-153;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
 QY 1 MGDHWSFLKDFLAGAANAASKTAVAPIERVKLLQVQASKOISAEKQYKGIIDCVVR 60
 DB 26 MTEQALISAFKDFLAGGIAAISKTAIVAPIERVKLLQVQASKOIADKQKGIIDCVVR 85
 QY 61 IPKEQGLSPFRGNLANVIRYFPFOALNPAFKDKYKQIFLGVDVRHKOFRYFAGNLASG 120
 DB 86 IPKEQGLSPFRGNLANVIRYFPFOALNPAFKDKYKQIFLGVDVRHKOFRYFAGNLASG 145

QY 121 GAAGATSLCFYYPIDPARRLAADVGR-AQREFHGLDCCIIFKSPDGLRGLYOGFNVS 179
 DB 146 GAAGATSLCFYYPIDPARRLAADVGRKSTEREFRGLDCLVKIKSDGIRGLYOGFNVS 205
 QY 180 VGGIITVRAAAYFGYVDTPAKGMLPDPKXNVHIFVSMNIAQSV-TAVAGLISYPPDT--VRR 239
 DB 206 VGGIITVRAAAYFGYVDTPAKGMLPDPKXNVHIFVSMNIAQSV-TAVAGLISYPPDTVRRMM 265
 QY 240 QSGRGADIMYTGVDCCWRKIAKDEGAKAFPKGAMSNVLRGMGAFVVLVDLKKVI 297
 DB 266 QSGRGADIMYTGVDCCWRKIFRDEGKAFPKGAMSNVLRGMGAFVVLVDLKKVI 323

RESULT 15

ABG15423
 ID ABG15423 standard; Protein; 325 AA.

AC ABG15423;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #15414.

KX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PP 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.

PA (HYSB-) HYSBQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.
 DR N-PSDB; AAS79610.

PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity

PS Claim 20; SEQ ID No 45782; 103bp; English.

CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pat_sequences.

XX SQ Sequence 325 AA;
 Query Match 83.4%; Score 1294.5; DB 22; Length 325;
 Best Local Similarity 83.4%; Pred. No. 8e-143;
 Matches 251; Conservative 19; Mismatches 26; Indels 5; Gaps 4;
 QY 1 MGDHAFSLKDFLAGAVALAAVSKTAVAPIERVKLLLOVQHASKQISAEKQYKGIIDCVR 60
 DB 24 MTDAAVSFAKDFLAGVAAAIKTAVAPIERVKLLLOVQHASKQIADKQYKGIIGCVR 83
 QY 61 IPKEQGLSFWRGVLAVIRFPTQALNFAKDKYKQIFLGVDNRHQFWRYPFAGNLASG 120
 DB 84 IPKEQGLSFWRGVLAVIRFPTQALNFAKDKYKQIFLGVDNRHQFWRYPFAGNLASG 143
 QY 121 GAAGATSLCFYYPIDPARRLAADVGR-AQREFHGLDCCIIFKSPDGLRGLYOGFNVS 179
 DB 144 GAAGATSLCFYYPIDPARRLAADVGRKSTEREFRGLDCLVKIKSDGIRGLYOGFNVS 203
 QY 180 VGGIITVRAAAYFGYVDTPAKGMLPDPKXNVHIFVSMNIAQSV-TAVAGLISYPPDT--VRR 236
 DB 204 VGGIITVRAAAYFGYVDTPAKGMLPDPKXNVHIFVSMNIAQSV-TAVAGLISYPPDTVRRMM 263
 QY 237 MMQSGRGADIMYTGVDCCWRKIAKDEGAKAFPKGAMSNVLRGMGAFVVLVDLKKVI 295
 DB 264 EXMQSGRGADIMYTGVDCCWRKIFRDEGKAFPKGAMSNVLRGMGAFVVLVDLKKVI 323
 QY 296 Y 296
 DB 324 Y 324

Search completed: December 18, 2003, 12:40:46
 Job time : 37.2542 secs

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2	1457.5	93.9	298	3	US-08-861-871-10	Sequence 10, Appl
3	1391.5	89.6	298	4	US-09-434-354-48	Sequence 48, Appl
4	1385.5	89.2	298	4	US-09-434-354-49	Sequence 49, Appl
5	304	19.6	469	4	US-09-996-243-289	Sequence 289, Appl
5	304	19.6	469	3	US-09-188-930-339	Sequence 339, Appl
6	301	19.4	469	4	US-09-312-283C-339	Sequence 339, Appl
7	301	19.4	469	4	US-09-160-113-4	Sequence 4, Appl
8	291	18.7	447	4	US-09-160-113-2	Sequence 2, Appl
9	291	18.7	447	4	US-09-482-272-118	Sequence 118, Appl
10	267	17.2	291	4	US-09-501-558-2	Sequence 12, Appl
11	265.5	17.1	335	4	US-08-333-750C-12	Sequence 12, Appl
12	238	15.3	320	3	US-09-434-613-12	Sequence 2, Appl
13	238	15.3	312	3	US-09-142-565-2	Sequence 56, Appl
14	233.5	15.0	312	3	US-08-470-878B-56	Sequence 56, Appl
15	227	14.6	299	1	US-08-470-878B-56	Sequence 51, Appl
16	227	14.6	299	2	US-08-518-878B-51	Sequence 51, Appl
17	227	14.6	309	1	US-08-807-861A-51	Sequence 51, Appl
18	227	14.6	309	2	US-08-807-861A-51	Sequence 51, Appl
19	227	14.6	309	2	US-08-910-681-51	Sequence 51, Appl
20	227	14.6	309	3	US-08-946-712A-51	Sequence 51, Appl
21	227	14.6	309	3	US-09-547-983-51	Sequence 51, Appl
22	227	14.6	311	2	US-08-775-009-33	Sequence 33, Appl
23	225	14.5	311	2	US-08-775-009-33	Sequence 33, Appl
24	222.5	14.3	308	2	US-09-172-528-2	Sequence 2, Appl
25	222.5	14.3	308	3	US-09-318-199-2	Sequence 2, Appl
26	222.5	14.3	308	3	US-09-318-199-2	Sequence 2, Appl
27	222.5	14.3	308	3	US-09-318-199-2	Sequence 2, Appl

45	190.5	12.5	306	5	PCT-US94-09799-1
44	192	12.4	303	4	US-09-547-983-37
43	192	12.4	303	3	US-08-946-719A-37
42	192	12.4	303	2	US-09-410-681-37
41	192	12.4	303	3	US-08-470-686A-37
40	192	12.4	303	2	US-08-807-861A-37
39	192	12.4	303	1	US-08-518-878B-37
38	193	12.4	303	1	US-08-294-522B-36
37	196.5	12.7	307	4	US-09-547-983-56
36	166.5	12.7	307	3	US-08-946-719A-56
35	166.5	12.7	307	3	US-09-420-681-56
34	166.5	12.7	307	2	US-08-807-861A-56
33	166.5	12.7	307	2	US-08-807-861A-56
32	166.5	12.7	307	1	US-08-946-719A-56
31	218.5	14.1	432	2	US-09-172-528-4
30	218.5	14.1	432	2	US-09-318-199-4
29	218.5	14.1	432	2	US-09-503-579-2
28	222.5	14.3	308	3	US-09-503-579-2
27	222.5	14.3	308	3	US-09-503-579-2
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25	222.5	14.3	308	3	US-09-503-579-2
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17	222.5	14.3	308	3	US-09-503-579-2
16	222.5	14.3	308	3	US-09-503-579-2
15	222.5	14.3	308	3	US-09-503-579-2
14	222.5	14.3	308	3	US-09-503-579-2
13	222.5	14.3	308	3	US-09-503-579-2
12	222.5	14.3	308	3	US-09-503-579-2
11	222.5	14.3	308	3	US-09-503-579-2
10	222.5	14.3	308	3	US-09-503-579-2
9	222.5	14.3	308	3	US-09-503-579-2
8	222.5	14.3	308	3	US-09-503-579-2
7	222.5	14.3	308	3	US-09-503-579-2
6	222.5	14.3	308	3	US-09-503-579-2
5	222.5	14.3	308	3	US-09-503-579-2
4	222.5	14.3	308	3	US-09-503-579-2
3	222.5	14.3	308	3	US-09-503-579-2
2	222.5	14.3	308	3	US-09-503-579-2
1	222.5	14.3	308	3	US-09-503-579-2

```

, RESULT 1
, US-09-434-354-47
, Sequence 47, Application US/09434354
, Patent No. 6562563
, GENERAL INFORMATION:
, APPLICANT: Murphy, Anne N.
, APPLICANT: Clevenger, William
, APPLICANT: Wiley, Sandra Ellen
, APPLICANT: Andreyev, Alexander Y.
, APPLICANT: Frigeri, Luciano G.
, APPLICANT: Vellicelbert, GonnI
, APPLICANT: Davis, Robert B.
, TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
, TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
, TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
, FILE REFERENCE: 660088_433
, CURRENT APPLICATION NUMBER: US/09/434,354
, CURRENT FILING DATE: 1999-11-03
, NUMBER OF SEQ. ID NOS: 54
, SOFTWARE: FastSeq for Windows Version 3.0
, SEQ ID NO 47
, LENGTH: 297
, TYPE: PRT
, ORGANISM: Homo sapien
, US-09-434-354-47

```

Query Match	100.0%;	Score 1553;	DB 4;	Length 297;
Best Local Similarity	100.0%;	Pred. No. 4.2e-172;		
Matches 297;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	1	MGHGAASFLKDFLAGVAAVAASKEKVAAPLERKLLILQYQHASKQISAEKQYKGIITDCYVR	60
Db	1	MGHGAASFLKDFLAGVAAVAASKEKVAAPLERKLLILQYQHASKQISAEKQYKGIITDCYVR	60
Qy	61	IPKQGFSLFWRGNLANVIRYPTQALNFAFKDKYIKQLFLGQVDRHKQFMWYFPAAGLASG	120
Db	61	IPKQGFSLFWRGNLANVIRYPTQALNFAFKDKYIKQLFLGQVDRHKQFMWYFPAAGLASG	120
Qy	121	GAGGAASLSECVPLDPAPKTRLLAADVGRRAQOBEPFGILGDCIIKIKPSQSLRSLYQGFVNSV	180
Db	121	GAGGAASLSECVPLDPAPKTRLLAADVGRRAQOBEPFGILGDCIIKIKPSQSLRSLYQGFVNSV	180
Qy	181	OGIIIVRAAYFGVYDTAKGMLDPDPKNVAHIFVSMNIAQSVTAAGILSLSPEDTVRRMMQ	240
Db	181	OGIIIVRAAYFGVYDTAKGMLDPDPKNVAHIFVSMNIAQSVTAAGILSLSPEDTVRRMMQ	240
Qy	241	SGKGAADIVYTQDNCMKRIADBEAKAPFGAGASNTLRGNGAPVULVDEIKCYV	297
Db	241	SGKGAADIVYTQDNCMKRIADBEAKAPFGAGASNTLRGNGAPVULVDEIKCYV	297

US-09-434-354-49

Query Match 89.2%; Score 1385.5; DB 4; Length 298;
Best Local Similarity 87.2%; Fred. No. 1.3e-152;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

Qy 1 MGDHMSLKDPLFGAVAAVSKTVAPIERVKLLIQVHASKQISAEKQYGIIDCVR 60
Db 1 MTEQALISAKDFLPGIIMAAISKTRVAIERVKLLIQVHASKQISADKQIKGIVDCLR 60
Qy 61 IPKQGLSPWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKKQFWRYFAGNLASG 120
Db 61 IPKQGLSPWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKKQFWRYFAGNLASG 120
Qy 121 GAAAGTSLCFYPPIDFATRLAADYGR-AQREFFGLDDCIITKFKSGMLGLYQGFVNS 179
Db 121 GAAAGTSLCFYPPIDFATRLAADYGR-AQREFFGLDDCIITKFKSGMLGLYQGFVNS 180
Qy 180 VQGIITVAAFGVYDIAKGMLEDPKQVHIFVSNMIAQSYTAVALSLSPEDTVRRRMM 239
Db 181 VQGIITVAAFGVYDIAKGMLEDPKQVHIFVSNMIAQSYTAVALSLSPEDTVRRRMM 240
Qy 240 QSGRKADIMYTGVDCKRKIAKDEGAKAFKGAWSNVLRGGAFLVLYDLKRV 297
Db 241 QSGRKADIMYTGVDCKRKIFRDEGKAFKGAWSNVLRGGAFLVLYDLKRV 298

RESULT 5
US-09-966-243-289

Sequence 289, Application US/09996243

Patent No. 6478825

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Deamoys, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerlitsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Grimaldi, Paul J.

APPLICANT: Gutney, Austin L.

APPLICANT: KJavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tuma, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730P1C13

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: US/09/996,243

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/087106

PRIOR FILING DATE: 1998-05-28

PRIOR APPLICATION NUMBER: 60/087607

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087609

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087759

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087827

PRIOR FILING DATE: 1998-06-03

PRIOR APPLICATION NUMBER: 60/088021

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088025

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088026

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088028

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088029

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088030

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088033

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088326

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088167

PRIOR FILING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: 60/088202

PRIOR FILING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: 60/088212

PRIOR FILING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: 60/088217

PRIOR FILING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: 60/088655

PRIOR FILING DATE: 1998-06-09

PRIOR APPLICATION NUMBER: 60/088734

PRIOR FILING DATE: 1998-06-10

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PRIOR FILING DATE: 1998-06-10

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PRIOR FILING DATE: 1998-06-10

PRIOR APPLICATION NUMBER: 60/088810

PRIOR FILING DATE: 1998-06-10

PRIOR APPLICATION NUMBER: 60/088824

PRIOR FILING DATE: 1998-06-10

PRIOR APPLICATION NUMBER: 60/088826

PRIOR FILING DATE: 1998-06-10

PRIOR APPLICATION NUMBER: 60/088858

PRIOR FILING DATE: 1998-06-11

PRIOR APPLICATION NUMBER: 60/088861

PRIOR FILING DATE: 1998-06-11

PRIOR APPLICATION NUMBER: 60/088876

PRIOR FILING DATE: 1998-06-11

PRIOR APPLICATION NUMBER: 60/089105

PRIOR FILING DATE: 1998-06-12

PRIOR APPLICATION NUMBER: 60/089440

PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/089512

PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/089514

PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/089532

PRIOR FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: 60/089538

PRIOR FILING DATE: 1998-06-17

PRIOR APPLICATION NUMBER: 60/089598

PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089601
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02

PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 19.6%; Score 304; DB 4; Length 469;
Best Local Similarity 29.0%; Pred. No. 1.4e-26;
Matches 88; Conservative 58; Mismatches 115; Indels 42; Gaps 11;

Qy 6 WSPFKDPLAGAAVAASKTAVAPIERVYLLQVGHASKQISAEKQYGIIDCVVRI 65
Db WRHL---VAGGGAAGAVERTCTAPLDRLKVMQV-HASR-----SNMNGIVGGFTQMI 237
Qy 66 GFISFMRGNLANVIRYPTQALNPAFKDKYKQFLGGVDR-----HKQFMRYPAGNTASG 120
Db GARSIMRGNINVLKIPESAIKFMAYEQIRLV--GSDQETLRHER-----LVAG 287
Qy 121 GAAGNTSLCFYPPDPARTRLAADVGRRAQREHFGLDCCIIRKSDGLRGLYGFNVSV 180
Db 288 SIAGIAIOSSITYEMEVKTRMAL---RKTGQYSGMDCAIRILAREGVAAPFYGYVPM 343
Qy 181 QGIIYRAAYGVYDTAKG-----LPPKVVHIFVSWMIASVYAVAGLSYPPDT 232
Db 344 LGIIFVAGIDLAIVETLKNMLOHYAVNSADP---GVVLACGTMSTCGQLASYPAL 400
Qy 233 VRRBMNQSGRKADIMYTGTVDCMRKIADGAKAPFKGMSVNLKMGAPV-LVLYD 291
Db 401 VRTMQAQSIEGAPFVYTMSSL--FKHILRTREGAFGLYRGLAPFMKVIYAVISISVYVE 458
Qy 292 EIK 294
Db 459 NLK 461

RESULT 6
US-09-188-930-339
Sequence 339; Application US/09188930A
Patent No. 6150502.
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Orlust, Rene
TITLE OF INVENTION: Compositions Isolated From Skin Cells
FILE REFERENCE: 11000.1011c1
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 339
LENGTH: 469
TYPE: PRT
ORGANISM: Mouse
US-09-188-930-339

Query Match 19.4%; Score 301; DB 3; Length 469;
Best Local Similarity 28.9%; Pred. No. 3e-26;
Matches 89; Conservative 64; Mismatches 103; Indels 52; Gaps 14;

Qy 6 WSPFKDPLAGAAVAASKTAVAPIERVYLLQVGHASKQISAEKQYGIIDCVVRI 61
Db 187 WRHL---VAGGGAAGAVERTCTAPLDRLKVMQV-HASRNSNM-----CIVGGFTQMI 233
Qy 62 PKGQGLSFMRGNLANVIRYPTQALNPAFKDKYKQFLGGVDR-----HKQFMRYPAGN 116

Db 234 IREGAGSLMKGNGINVLKIPESAIKPMAYEQMKRLV--GSDQETLRIHER----- 283
Qy 117 LASGAAGATSLCVCVPLDFAKRLADVGRRAQREHFGDLCIKIKFKSGLAGLYOGF 176
Db 284 LVASGLAGALAOSSITYPEMEVILKTRMAL--RTKGQYSGLMDCKRRIIAKGVAAFAFKGY 339
Qy 177 NVSVGGIITRYAAVFGVYDTAKGM-----LPPDKNVHIFVSMMLAQSOTAAVAG--LIS 227
Db 340 IPNMLGIIPVAGIDILAVETIKNTWLORYAVNSADP---GVFV--LACGTTISSTCGQLAS 395
Qy 228 YPFPTVRRMMQSGRKADIMYTGTVDCMKRIADBGAKAFPKGANSVLRKMGAGAFV- 286
Db 396 YPLALVTRMQAQSIEGAPETWSSL--FKQILRTBGAFLYRGLAPNFKVIPAISIS 453
Qy 287 LVLYDEIK 294
Db 454 YVYVENLK 461

RESULT 7

US-09-312-283C-339
; Sequence 339, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Muriison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312, 283C
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 339
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-339

Query Match 19.4%; Score 301; DB 4; Length 469;
Best Local Similarity 28.9%; Pred. No. 3e-26;
Matches 89; Conservative 64; Mismatches 103; Indels 52; Gaps 14;
Qy 6 WSPFLKDFLAGAANAASKTAAVAPIERVLLQVOHASKQISAEKQYKGIIDCVV----RI 61
Db 187 WRHL---VAGGAGAVSRTCTAPLDRLKVLMOV--HASSNNM-----CIVGGFTQM 233
Qy 62 PKEQPLSPWGNLANVIRYPTQALNFAFDKTKQFLGVDV----HKQFWRYPAGN 116
Db 234 IREGAGSLMKGNGINVLKIPESAIKPMAYEQMKRLV--GSDQETLRIHER----- 283
Qy 117 LASGAAGATSLCVCVPLDFAKRLADVGRRAQREHFGDLCIKIKFKSGLAGLYOGF 176
Db 284 LVASGLAGALAOSSITYPEMEVILKTRMAL--RTKGQYSGLMDCKRRIIAKGVAAFAFKGY 339
Qy 177 NVSVGGIITRYAAVFGVYDTAKGM-----LPPDKNVHIFVSMMLAQSOTAAVAG--LIS 227
Db 340 IPNMLGIIPVAGIDILAVETIKNTWLORYAVNSADP---GVFV--LACGTTISSTCGQLAS 395
Qy 228 YPFPTVRRMMQSGRKADIMYTGTVDCMKRIADBGAKAFPKGANSVLRKMGAGAFV- 286
Db 396 YPLALVTRMQAQSIEGAPETWSSL--FKQILRTBGAFLYRGLAPNFKVIPAISIS 453
Qy 287 LVLYDEIK 294
Db 454 YVYVENLK 461

RESULT 8

US-09-160-119-4
; Sequence 4, Application US/09160119A
; Patent No. 6316219
; GENERAL INFORMATION:
; APPLICANT: KRIEF, STEPHANE
; APPLICANT: SOUCHET, MICHEL
; APPLICANT: BRILL, ANTOINE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30985
; CURRENT APPLICATION NUMBER: US/09/160, 119A
; CURRENT FILING DATE: 1998-09-24
; EARLIER APPLICATION NUMBER: EP 97402511.6
; EARLIER FILING DATE: 1997-10-23
; EARLIER APPLICATION NUMBER: EP 98401655.0
; EARLIER FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 447
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-160-119-4

Query Match 18.7%; Score 291; DB 4; Length 447;
Best Local Similarity 27.5%; Pred. No. 4.1e-25;
Matches 80; Conservative 53; Mismatches 136; Indels 22; Gaps 7;
Qy 12 FLAGAANAASKTAAVAPIERVLLQVOHASKQISAEKQYKGIIDCVRIPEKQPLSEW 71
Db 104 FGLGSVAGAVGATVYVIDVITKTMQNRSTGSFVGLIMYKNSPDCFKVLRYGFFGLY 163
Qy 72 RGNLANVIRYPTQALNFAFDKTKQFLGVDVRRHKQPMKRYFAGNLSAGGAATSLCFV 131
Db 164 RGLLPOLGVAPEKAIKLYNDVFRDKFM---HXGQSVPLAEIILAGGCGAGSQTFT 218
Qy 132 YPLDFAKRL--AADV--GRRAGREHFGDLCIKIKFKSGLAGLYOGFNVSVGGIITRY 187
Db 219 NPELIVYKIRLQVAGEITTGRRVS-----ALSVRDGFFGRIYKAGACFLRDLIFS 269
Qy 188 AAYFGVYDTAKGMLPDRKNVHIFVSMMLAQSOTAAV--AGLLSYPTVRRMMQSGRKA 246
Db 270 AIYPPCYAHVYASFANDQGVSPGSLILAGAIAGMPAASIVTPADVITKR--LQVAARAG 327
Qy 247 DIWTVGVDCMKRIADBGAKAFPKGANSVLRKMG--APVLYYDEIKKY 296
Db 328 QTTYSVVIDCFKRLREBGPALMKGAGAVFSSSPQGVTLTYELLQRW 378

RESULT 9

US-09-160-119-2
; Sequence 2, Application US/09160119A
; Patent No. 6316219
; GENERAL INFORMATION:
; APPLICANT: KRIEF, STEPHANE
; APPLICANT: SOUCHET, MICHEL
; APPLICANT: BRILL, ANTOINE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30985
; CURRENT APPLICATION NUMBER: US/09/160, 119A
; CURRENT FILING DATE: 1998-09-24
; EARLIER APPLICATION NUMBER: EP 97402511.6
; EARLIER FILING DATE: 1997-10-23
; EARLIER APPLICATION NUMBER: EP 98401655.0
; EARLIER FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 674
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-160-119-2

Query Match 18.7%; Score 291; DB 4; Length 674;

Best Local Similarity 27.5%; Pred. No. 7.7e-25;
Matches 80; Conservative 53; Mismatches 136; Indels 22; Gaps 7;

QY 12 FLAGAANAASVETAPAPIERVELLLQVQASKOISAEQYKGIIDCVIRPEOGLTFM 71
DB 331 FGLSVAAGVATVATVPIDVLTQKTRQNGRSTQSPFGLMNTKNSPFCFKVLRYSBEFLX 390
QY 72 RGNLANVIRYPPQALNPAFKDKYKQLFLGGVDRHKQFWRYPAGNLASGAAGATSLCFV 131
DB 391 RGLLPOLLGVAPEKAIKLTVDVFDKTFM-----HKDGSVPLAAILLAGGAGGSGQVIFT 445
QY 132 YPLDPAFRL--AADV--GRRAQRFHGLDGIITIKFSDGLRGVYQGFNNVSGIITXR 187
DB 446 NPLEIVKIRLQVAGSITTPRVS-----ALSVDLGFPGIYKAKACFLTDIPFS 496
QY 188 AAFGVYDTAKGMLDPPKQVHIFVSMIAQSVTAV-AGLLSYFPTVRRMMQSGRKGA 246
DB 497 AIFPCVAVKASPNEDGQVSPGSLLAGALAGPAASTVTPADVITR--LQVAAAG 554
QY 247 DIMTGTVDCKRKIAKDEGAKAFPKGANSVLRGKG-APVLVLYDEIKY 296
DB 555 QTVSGVIDCPRKILREBGPALMKAGARVRSPPQGVTLITVELQRW 605

RESULT 10
US-09-501-558-2
Sequence 2, Application US/09501558
Patent No. 6403784
GENERAL INFORMATION:
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Mathur, Brian
APPLICANT: Zambrowicz, Brian
TITLE OF INVENTION: No. 6403784e1 Human Uncoupling Proteins and
FILE REFERENCE: LEX-0012-USA
CURRENT APPLICATION NUMBER: US/09/501,558
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 291
TYPE: PRT
ORGANISM: Homo sapiens
US-09-501-558-2

Query Match 17.2%; Score 267; DB 4; Length 291;
Best Local Similarity 28.4%; Pred. No. 1.3e-22;
Matches 84; Conservative 51; Mismatches 137; Indels 24; Gaps 9;

QY 10 KDFLAGAANAASVETAPAPIERVELLLQVQASKOIS-AEQYKGIIDCVIRPEOGL 68
DB 7 KPFYVGLASITAEGETFPIDVLTQKTRQNGRSTQSPFGLMNTKNSPFCFKVLRYSBEFLX 66
QY 69 SFWRGNLANVIRYPPQALNPAFKDKYKQLFLGGVDRHKQFWRYPAGNLASGAAGATSL 128
DB 67 AYSGLAPAMLRQASVGTIKIGTYSGLKRLF---TERED--ETLPINIVIGIISGVIS 121
QY 129 CFVYPLDPAFRTADVGRRAQRFHGLDGIITIKFSDGLRGVYQGFNNVSGIITXR 188
DB 122 TIANFTDVLTQKTRQNGRSTQSPFGLMNTKNSPFCFKVLRYSBEFLX 177
QY 189 AAFGVYDTAK-----GMLPDPKQVHIFVSMIAQSVTAVAG-LLSYFPTVRRMMQ 241
DB 178 VELPVPYDITKQKHLISGMGDTILTR-----TGLGALASNPVDVTRMMQ 232
QY 242 G-RKADIMTGTVDCKRKIAKDEGAKAFPKGANSVLR-GMGAPVLVLYDEIKY 295
DB 233 VLDRGRCGSGYGTIDCLLQVQASKOISAEQYKGIIDCVIRPEOGLTFM 288

RESULT 11
US-09-482-273-118

Sequence 118, Application US/09482273
Patent No. 6534631
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: P2030P1
CURRENT APPLICATION NUMBER: US/09/482,273
EARLIER FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,922
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,956
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 118
LENGTH: 335
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (335)
OTHER INFORMATION: Xaa equals stop translation
US-09-482-273-118

Query Match 17.1%; Score 265.5; DB 4; Length 335;
Best Local Similarity 30.0%; Pred. No. 2.4e-22;
Matches 89; Conservative 43; Mismatches 138; Indels 27; Gaps 10;

QY 10 KDFLAGAANAASVETAPAPIERVELLLQVQASKOIS--EQYKGIIDCVIRPEOGL 66
DB 51 KPFYVGLASITAEGETFPIDVLTQKTRQNGRSTQSPFGLMNTKNSPFCFKVLRYSBEFLX 108
QY 67 FLSTWRGNLANVIRYPPQALNPAFKDKYKQLFLGGVDRHKQFWRYPAGNLASGAAGAT 126
DB 109 VLAYSGLAPALNPAFKDKYKQLFLGGVDRHKQFWRYPAGNLASGAAGAT 163
QY 127 SLCFVYPLDPAFRTADVGRRAQRFHGLDGIITIKFSDGLRGVYQGFNNVSGIITXR 186
DB 164 SSTIANFTDVLTQKTRQNGRSTQSPFGLMNTKNSPFCFKVLRYSBEFLX 219
QY 187 AAFGVYDTAK-----GMLPDPKQVHIFVSMIAQSVTAVAG-LLSYFPTVRRMMQ 239
DB 220 VGVLPYDITKQKHLISGMGDTILTR-----FVSFTGLAGALASNPVDVTRMMQ 274
QY 240 QSGRKADIMTGTVDCKRKIAKDEGAKAFPKGANSVLR-GMGAPVLVLYDEIKY 295
DB 275 QRAIVGHVDLVKGTVDGILKMKHKBGFPALYKGFPMNVLRLGPMNIIFFIYELQK 331

RESULT 12
US-08-933-750C-12
Sequence 12, Application US/08933750C
Patent No. 5932442
GENERAL INFORMATION:
APPLICANT: Lal, Preeti.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shan, Putvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA

RESULT 13
 US-09-234-613-12
 : Sequence 12, Application US/09234613
 : Patent No. 6132973
 : GENERAL INFORMATION:
 :
 : APPLICANT: Lal, Preeti
 : APPLICANT: Hillman, Jennifer L.
 : APPLICANT: Bandman, Olga
 : APPLICANT: Shah, Fuvri
 : APPLICANT: Au-Young, Janice
 : APPLICANT: Yue, Henry

```

Oy      1  IAAVAAASKTAAVPIEBVKLLQVOHAS--KQISAEKQYGGIIDCVARIKKEGGLSPF  71
Db      20 VAGSVGGLVTRALISFPYDIKIRFQDQHERLSRSDPSAKYHGIIQASRQILQEBGPFAFM  79

Oy      72 KGNLANVIRYFPTQALNF-AFKDKYKKQLFLGQVDRHKKQFWRYFAGNLASGGAAGATSLCF  130
Db      80 KGHVPPQIIISIGYGAVOFLSEFEMLTETLHRSVSVDAREFSVHF----VCGGLAACVATLT  135

Oy      131 VYPLDPARTRLADYVGRARQOREFHGLEDGCIKIFPSDGLRGLYOGFNVSVOGIIYYAAV  180
Db      136 VHVVDVLTKRFPAA---QSEPKRYNTLRLRAVGTMRSEDPQYFYGLAPTLIAIFPPYGLQ  192

Oy      191 EGVYDTAKGMLDPPKKNVHIFVSWMI-----AQSVTAAGLISPEPTVRR  235
Db      193 FSCYCSLTK-----HDY-KMALPAEKINENIQLNLCSGGAGVSKITLYPLDIEFKK  242

Oy      236 RMMQ-----QSGRK--GADIMYTGTVDSKIKANDGAKAPFGAASNYLR--GMGAPFLVLT  289
Db      243 RLQVGGFEHRAARAFQVYRRYKGLMDCAQVQLQEGAGLGFPGKLSPSLLKALSTGFMFPS  302

Oy      290 YD 291
Db      303 YE 304

```

RESULT 14
US-09-142-565-2

```

; Sequence 2, Application US/09142565A
; Patent No. 6187560
; GENERAL INFORMATION:
; APPLICANT: Lee James Beeley
; APPLICANT: Kelly Paine
; APPLICANT: Robert James
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30002
; CURRENT APPLICATION NUMBER: US/09/142,565A
; CURRENT FILING DATE: 1999-06-30
; EARLIER APPLICATION NUMBER: 9704551.2
; EARLIER FILING DATE: 1997-03-05
; EARLIER APPLICATION NUMBER: 9705614.7
; EARLIER FILING DATE: 1997-03-18
; EARLIER APPLICATION NUMBER: 97305305.1
; EARLIER FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
US-09-142-565-2

Query Match      15.0%; Score 233.5; DB 3; Length 312;
Best Local Similarity 24.7%; Pred. No. 1.2e-18;
Matches 73; Conservative 53; Mismatches 145; Indels 25; Gaps 8;

QY 12 FLAGAANAASKTAVAPIERYVLLQVOHASK--QYKGIIDCVVRIPKEQFLS 69
DB 17 FLAGCTAACFADLTFFLDITAKVRLQIQSGSPVRAVTSQYHGWGTLITWRTSGPR 76
QY 70 FWRGNLANVIRYFPPTQALNFAFKDKYKQFL-GGVDRHKQFWRYPAGNLASGAAGATSL 128
DB 77 PYNGLVAGLQROMSPASIRIGLYDSVKQYTPKGDNSLTLRLA-----GCTTGAMAV 131
QY 129 CFVYPLDPAIRLADV---GRRARERHGLGDCIIKIFKSDGLGLYOGFNVSVQGIIT 185
DB 132 TCAOPTDVVKVRFQAPASIHGSPRSRDKYSGTMDAYRTIAREBGVGLWKTLPNIRNAI 191
QY 186 YRAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTA-----VAGLSYFPDVRBRMMQ 240
DB 192 VNCAEVVYTDILKEKLD---YHLTDFNPFCHFVSAFAGAFYVAVSPVDVVKRYM-- 246
QY 241 SGRKADIMYTGVDGWRKIANDGAKAFPKGAMSNVLR-GMGAFVLYLVYDEIKK 295
DB 247 ---NSPPQGYSPDLCMKVNAQEGPTAFYKGFSTPSFLRSGMNVVMFVTEQLKR 299

RESULT 15
US-08-518-878B-56
; Sequence 56, Application US/08518878B
; Patent No. 5702902
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pennie & Edwards
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/518,878B
; FILING DATE: 23-AUG-1995

```

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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEFAX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 299 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
US-08-518-878B-56

Query Match      14.6%; Score 227; DB 1; Length 299;
Best Local Similarity 23.8%; Pred. No. 6.2e-18;
Matches 70; Conservative 52; Mismatches 148; Indels 24; Gaps 7;

QY 12 FLAGAANAASKTAVAPIERYVLLQVOHASK--QISAEKQYKGIIDCVVRIPKEQFL 68
DB 7 FLAGCTAACFADLTFFLDITAKVRLQIQSGSPVRAVTSQYHGWGTLITWRTSGPR 66
QY 69 SFRGNLANVIRYFPPTQALNFAFKDKYKQFLGGVDRHKQFWRYPAGNLASGAAGATSL 128
DB 67 SLVNGLVAGLQROMSPASIRIGLYDSVKQFYTKGSEHAS-----IGSRLLAGSTTGALAV 121
QY 129 CFVYPLDPAIRLADVGRARERHGLGDCIIKIFKSDGLGLYOGFNVSVQGIIT 188
DB 122 AVAOPTDVVKVRFQAPASIHGSPRSRDKYSGTMDAYRTIAREBGVGLWKTLPNIRNAI 181
QY 189 AYFGVYDTAK-----GMLPDPKNVHIFVSWMIAQSVTAAGLSYFPDVRBRMMQSG 242
DB 182 AELVYTDILQALDKANLMTDLDLFCF-FTSAFAGFCTTV---IASVDVVKRYM----- 233
QY 243 RKGADIMYTGVDGWRKIANDGAKAFPKGAMSNVLR-GMGAFVLYLVYDEIKK 295
DB 234 -NSALQGYSSAGHCALTMLQKEGPRAFYKGFMPSEFLRSGMNVVMFVTEQLKR 286

Search completed: December 18, 2003, 12:44:54
Job time : 13.3057 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:43:17 ; Search time 24.2768 Seconds
(without alignments)
2284.595 Million cell updates/sec

Title: US-09-811-131-31

Perfect score: 1553
Sequence: 1 MGHASFLKDFLAGVA...LRGAGAFVLYDEIKKY 297

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubppaa/PCR_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*
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- 14: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep:*
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- 18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	1553	100.0	297	9 US-09-811-094-31	Sequence 31, Appl
2	1553	100.0	297	9 US-09-810-644-31	Sequence 31, Appl
3	1553	100.0	297	10 US-09-185-904A-31	Sequence 31, Appl
4	1391.5	89.6	298	9 US-09-811-094-32	Sequence 32, Appl
5	1391.5	89.6	298	9 US-09-810-644-32	Sequence 32, Appl
6	1391.5	89.6	298	10 US-09-185-904A-32	Sequence 32, Appl
7	1385.5	89.2	298	9 US-09-811-094-33	Sequence 33, Appl
8	1385.5	89.2	298	9 US-09-810-644-33	Sequence 33, Appl
9	1385.5	89.2	298	10 US-09-185-904A-33	Sequence 33, Appl
10	773.5	49.6	179	12 US-10-029-386-32501	Sequence 32501, A
11	773.5	49.6	179	12 US-10-032-585-7194	Sequence 7194, Ap
12	740	47.6	381	12 US-10-141-478A-2	Sequence 2, Appl
13	734	47.3	318	10 US-09-801-368-252	Sequence 252, Appl
14	734	47.3	386	9 US-09-734-569-170	Sequence 170, App
15	703.5	45.3	308	15 US-10-128-714-3338	Sequence 3338, Ap

16	703.5	45.3	308	15	US-10-128-714-8338	Sequence 8338, Ap
17	666	42.9	677	12	US-10-259-165-192	Sequence 192, App
18	461	29.7	132	9	US-09-825-301-1459	Sequence 1459, App
19	402.5	25.9	87	9	US-09-864-761-36440	Sequence 36440, A
20	350.5	22.6	475	10	US-09-777-921A-4	Sequence 4, Appl1
21	346.5	22.3	477	10	US-09-777-921A-2	Sequence 2, Appl1
22	320.5	20.6	384	12	US-10-094-749-1789	Sequence 1789, Ap
23	312	20.1	410	10	US-09-777-921A-5	Sequence 5, Appl1
24	306	19.7	680	12	US-10-291-172-339	Sequence 339, App
25	304	19.6	469	9	US-09-989-722-289	Sequence 289, App
26	304	19.6	469	9	US-09-989-723-289	Sequence 289, App
27	304	19.6	469	9	US-09-989-279-289	Sequence 289, App
28	304	19.6	469	9	US-09-989-727-289	Sequence 289, App
29	304	19.6	469	10	US-09-989-731-289	Sequence 289, App
30	304	19.6	469	10	US-09-989-732-289	Sequence 289, App
31	304	19.6	469	10	US-09-991-073-289	Sequence 289, App
32	304	19.6	469	10	US-09-990-442-289	Sequence 289, App
33	304	19.6	469	10	US-09-991-163-289	Sequence 289, App
34	304	19.6	469	10	US-09-993-604-289	Sequence 289, App
35	304	19.6	469	10	US-09-990-456-289	Sequence 289, App
36	304	19.6	469	10	US-09-989-721-289	Sequence 289, App
37	304	19.6	469	10	US-09-992-596-289	Sequence 289, App
38	304	19.6	469	10	US-09-989-735-289	Sequence 289, App
39	304	19.6	469	10	US-09-989-735-289	Sequence 289, App
40	304	19.6	469	10	US-09-990-444-289	Sequence 289, App
41	304	19.6	469	10	US-09-991-181-289	Sequence 289, App
42	304	19.6	469	10	US-09-989-730-289	Sequence 289, App
43	304	19.6	469	10	US-09-990-436-289	Sequence 289, App
44	304	19.6	469	10	US-09-993-687-289	Sequence 289, App
45	304	19.6	469	11	US-09-989-734-289	Sequence 289, App

ALIGNMENTS

RESULT 1
US-09-811-094-31
Sequence 31, Application US/09811094
Patent No. US2001004144A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert R.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yashong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D4
CURRENT APPLICATION NUMBER: US/09/811, 094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 31
LENGTH: 297
TYPE: PRT
ORGANISM: Homo sapien
US-09-811-094-31

Query Match 100.0%; Score 1553; DB 9; Length 297;
Best Local Similarity 100.0%; Pred. No. 2.3e-160;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGHASFLKDFLAGVA...LTVAPLERYVLLQVGHASQISAQKQKIIIDCVR 60
DB 1 MGHASFLKDFLAGVA...LTVAPLERYVLLQVGHASQISAQKQKIIIDCVR 60
QY 1 IPKGGFLSFWKGNLNVIRYPTQALNFAFKQKQKQLFGGVDRHKQFRRYPAGNLAAG 120
DB 61 IPKGGFLSFWKGNLNVIRYPTQALNFAFKQKQKQLFGGVDRHKQFRRYPAGNLAAG 120

QY 121 GAAGTSLCFYVPLDPARTRLADVGRRAQREHFHGLDCCIIRKFSDELRLGLYOGFNVS 180
 DB 121 GAAGTSLCFYVPLDPARTRLADVGRRAQREHFHGLDCCIIRKFSDELRLGLYOGFNVS 180
 QY 181 OGIIITRAYRGVYDTAKGMLPDPKNVHI FVSWMTAOSTAVAGLLSTPFTVRRMMQ 240
 DB 181 OGIIITRAYRGVYDTAKGMLPDPKNVHI FVSWMTAOSTAVAGLLSTPFTVRRMMQ 240
 QY 241 SGRKADIMYGTVDGCMRKIADEGAKAFKFGAMSNVLRMGGAFLVLYDEIKKYV 297
 DB 241 SGRKADIMYGTVDGCMRKIADEGAKAFKFGAMSNVLRMGGAFLVLYDEIKKYV 297

RESULT 2

US-09-810-644-31
 ; Sequence 31, Application US/09810644
 ; Patent No. US20020012992A1

GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.
 APPLICANT: Davis, Robert E.
 APPLICANT: Clevenger, William
 APPLICANT: Wiley, Sandra Eileen
 APPLICANT: Miller, Scott W.
 APPLICANT: Szabo, Tomas R.
 APPLICANT: Ghosh, Soumitra S.
 APPLICANT: Moos, Walter H.
 APPLICANT: Pel, Yazhong
 TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
 TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
 FILE REFERENCE: 660088.420D3
 CURRENT FILING DATE: 2001-03-14
 NUMBER OF SEQ ID NOS: 37
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 31
 LENGTH: 297
 TYPE: PRT
 ORGANISM: Homo sapien
 US-09-810-644-31

Query Match 100.0%; Score 1553; DB 9; Length 297;
 Best Local Similarity 100.0%; Pred. No. 2.3e-160;
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHMSFLKDFLAGAVALAAVSKTAVAPIERVKLLQVQHASKQISAEKQYGIIDCVR 60
 DB 1 MGDHMSFLKDFLAGAVALAAVSKTAVAPIERVKLLQVQHASKQISAEKQYGIIDCVR 60
 QY 61 IPKEGFLSFWRGMLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKKQFWRYPAGNLASG 120
 DB 61 IPKEGFLSFWRGMLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKKQFWRYPAGNLASG 120
 QY 121 GAAGTSLCFYVPLDPARTRLADVGRRAQREHFHGLDCCIIRKFSDELRLGLYOGFNVS 180
 DB 121 GAAGTSLCFYVPLDPARTRLADVGRRAQREHFHGLDCCIIRKFSDELRLGLYOGFNVS 180
 QY 181 OGIIITRAYRGVYDTAKGMLPDPKNVHI FVSWMTAOSTAVAGLLSTPFTVRRMMQ 240
 DB 181 OGIIITRAYRGVYDTAKGMLPDPKNVHI FVSWMTAOSTAVAGLLSTPFTVRRMMQ 240
 QY 241 SGRKADIMYGTVDGCMRKIADEGAKAFKFGAMSNVLRMGGAFLVLYDEIKKYV 297
 DB 241 SGRKADIMYGTVDGCMRKIADEGAKAFKFGAMSNVLRMGGAFLVLYDEIKKYV 297

RESULT 3

US-09-185-904A-31
 ; Sequence 31, Application US/09185904A
 ; Patent No. US2002017185A1

GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.
 APPLICANT: Davis, Robert E.

APPLICANT: Clevenger, William
 APPLICANT: Wiley, Sandra Eileen
 APPLICANT: Miller, Scott W.
 APPLICANT: Szabo, Tomas R.
 APPLICANT: Ghosh, Soumitra S.
 APPLICANT: Moos, Walter H.
 APPLICANT: Pel, Yazhong
 TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
 TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
 FILE REFERENCE: 660088.420
 CURRENT FILING DATE: 1998-11-03
 NUMBER OF SEQ ID NOS: 33
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 31
 LENGTH: 297
 TYPE: PRT
 ORGANISM: Homo sapien
 US-09-185-904A-31

Query Match 100.0%; Score 1553; DB 10; Length 297;
 Best Local Similarity 100.0%; Pred. No. 2.3e-160;
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHMSFLKDFLAGAVALAAVSKTAVAPIERVKLLQVQHASKQISAEKQYGIIDCVR 60
 DB 1 MGDHMSFLKDFLAGAVALAAVSKTAVAPIERVKLLQVQHASKQISAEKQYGIIDCVR 60
 QY 61 IPKEGFLSFWRGMLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKKQFWRYPAGNLASG 120
 DB 61 IPKEGFLSFWRGMLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKKQFWRYPAGNLASG 120
 QY 121 GAAGTSLCFYVPLDPARTRLADVGRRAQREHFHGLDCCIIRKFSDELRLGLYOGFNVS 180
 DB 121 GAAGTSLCFYVPLDPARTRLADVGRRAQREHFHGLDCCIIRKFSDELRLGLYOGFNVS 180
 QY 181 OGIIITRAYRGVYDTAKGMLPDPKNVHI FVSWMTAOSTAVAGLLSTPFTVRRMMQ 240
 DB 181 OGIIITRAYRGVYDTAKGMLPDPKNVHI FVSWMTAOSTAVAGLLSTPFTVRRMMQ 240
 QY 241 SGRKADIMYGTVDGCMRKIADEGAKAFKFGAMSNVLRMGGAFLVLYDEIKKYV 297
 DB 241 SGRKADIMYGTVDGCMRKIADEGAKAFKFGAMSNVLRMGGAFLVLYDEIKKYV 297

RESULT 4

US-09-811-094-32
 ; Sequence 32, Application US/09811094
 ; Patent No. US2001004414A1

GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.
 APPLICANT: Davis, Robert E.
 APPLICANT: Clevenger, William
 APPLICANT: Wiley, Sandra Eileen
 APPLICANT: Miller, Scott W.
 APPLICANT: Szabo, Tomas R.
 APPLICANT: Ghosh, Soumitra S.
 APPLICANT: Moos, Walter H.
 APPLICANT: Pel, Yazhong
 TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
 TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
 FILE REFERENCE: 660088.420D4
 CURRENT FILING DATE: 2001-03-14
 NUMBER OF SEQ ID NOS: 37
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 32
 LENGTH: 298
 TYPE: PRT
 ORGANISM: Homo sapien
 US-09-811-094-32

Query Match 89.6%; Score 1391.5; DB 9; Length 298;
 Best Local Similarity 88.6%; Pred. No. 8.3e-143;

Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

Qy 1 MGDHMSFLKDFLAGAAGAAVSKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVR 60
Db 1 MTDALSLAKDFLAGAAGAAVSKTAVAPIERVKLLQVQHASKOITADKQYKGIIDCVR 60

Qy 61 IPKEQGLSPFRGNLANVIRYPTQALNFAFKDKYKOLFLGGVDRHKOFRMYFAGNLASG 120
Db 61 IPKEQGLSPFRGNLANVIRYPTQALNFAFKDKYKOLFLGGVDRHKOFRMYFAGNLASG 120

Qy 121 GAAGATSLCFYYPPLDPARTRLAADVGR-ADREPHGLDCCIIFKSDGLRGLYQGFNV 179
Db 121 GAAGATSLCFYYPPLDPARTRLAADVGR-ADREPHGLDCCIIFKSDGLRGLYQGFNV 180

Qy 180 VGGIIYRAAYFGYDPAKGMPLDPKXNHIFVSMIAOSTYAVAGLSTYPTDTRRRMM 239
Db 180 VGGIIYRAAYFGYDPAKGMPLDPKXNHIFVSMIAOSTYAVAGLSTYPTDTRRRMM 240

Qy 240 QSGRKGADIMYTGVDCKRIAKDEGAKAFKGAWSNVLKMGAFVLVLYDEIKKY 296
Db 241 QSGRKGADIMYTGVDCKRIAKDEGAKAFKGAWSNVLKMGAFVLVLYDEIKKY 297

RESULT 5
US-09-810-644-32
Sequence 32, Application US/09810644
Patent No. US2002012992A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Willet, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pel, Yashong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D3
CURRENT APPLICATION NUMBER: US/09/810.644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-810-644-32

Query Match 89.6%; Score 1391.5; DB 9; Length 298;
Best Local Similarity 88.6%; Pred. No. 8.3e-143;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

RESULT 6
US-09-185-904A-32
Sequence 32, Application US/09185904A
Patent No. US20020177185A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Willet, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pel, Yashong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 660088.420
CURRENT APPLICATION NUMBER: US/09/185.904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-185-904A-32

Query Match 89.6%; Score 1391.5; DB 10; Length 298;
Best Local Similarity 88.6%; Pred. No. 8.3e-143;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

Qy 1 MGDHMSFLKDFLAGAAGAAVSKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVR 60
Db 1 MTDALSLAKDFLAGAAGAAVSKTAVAPIERVKLLQVQHASKOITADKQYKGIIDCVR 60

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Db 61 IPKEQGLSPFRGNLANVIRYPTQALNFAFKDKYKOLFLGGVDRHKOFRMYFAGNLASG 120

Qy 121 GAAGATSLCFYYPPLDPARTRLAADVGR-ADREPHGLDCCIIFKSDGLRGLYQGFNV 179
Db 121 GAAGATSLCFYYPPLDPARTRLAADVGR-ADREPHGLDCCIIFKSDGLRGLYQGFNV 180

Qy 180 VGGIIYRAAYFGYDPAKGMPLDPKXNHIFVSMIAOSTYAVAGLSTYPTDTRRRMM 239
Db 180 VGGIIYRAAYFGYDPAKGMPLDPKXNHIFVSMIAOSTYAVAGLSTYPTDTRRRMM 240

Qy 240 QSGRKGADIMYTGVDCKRIAKDEGAKAFKGAWSNVLKMGAFVLVLYDEIKKY 296
Db 241 QSGRKGADIMYTGVDCKRIAKDEGAKAFKGAWSNVLKMGAFVLVLYDEIKKY 297

RESULT 7
US-09-811-094-33
Sequence 33, Application US/09811094
Patent No. US2001004414A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Willet, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pel, Yashong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D4
CURRENT APPLICATION NUMBER: US/09/811.094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-811-094-33

Query Match 89.2%; Score 1385.5; DB 9; Length 298;
Best Local Similarity 87.2%; Pred. No. 3.7e-142;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYGIIDCVR 60
DB 1 MTEQALSPKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYGIIDCVR 60
QY 61 IPKEGGLSPFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDHKKQFWRYPAGNLASG 120
DB 61 IPKEGGLSPFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDHKKQFWRYPAGNLASG 120
QY 121 GAAGATSLCFVYPLDPARTRLAADVGR-AGREFHGLDCCIIFKSDGLRGLYQGFVS 179
DB 121 GAAGATSLCFVYPLDPARTRLAADVGR-AGREFHGLDCCIIFKSDGLRGLYQGFVS 180
QY 180 VGGIIYRAAFVGYVDTAKGMLPDKNVHIFVSMIAQSVTAAGLLSYPTVRRMM 239
DB 180 VGGIIYRAAFVGYVDTAKGMLPDKNVHIFVSMIAQSVTAAGLLSYPTVRRMM 240
QY 240 QSGRKGADIMYTGVDCKRKIADEGAKAFPKGAMSVNLKMGCAFVLVYDELKCV 297
DB 241 QSGRKGADIMYTGVDCKRKIFRDEGKAFPKGAMSVNLKMGCAFVLVYDELKCV 298

RESULT 8

US-09-810-644-33
Sequence 33, Application US/09810644
Patent No. US20020012992A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Willey, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pel, Yashong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D3
CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-810-644-33

Query Match 89.2%; Score 1385.5; DB 9; Length 298;
Best Local Similarity 87.2%; Pred. No. 3.7e-142;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYGIIDCVR 60
DB 1 MTEQALSPKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYGIIDCVR 60
QY 61 IPKEGGLSPFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDHKKQFWRYPAGNLASG 120
DB 61 IPKEGGLSPFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDHKKQFWRYPAGNLASG 120
QY 121 GAAGATSLCFVYPLDPARTRLAADVGR-AGREFHGLDCCIIFKSDGLRGLYQGFVS 179
DB 121 GAAGATSLCFVYPLDPARTRLAADVGR-AGREFHGLDCCIIFKSDGLRGLYQGFVS 180

DB 121 GAAGATSLCFVYPLDPARTRLAADVGR-AGREFHGLDCCIIFKSDGLRGLYQGFVS 180
QY 180 VGGIIYRAAFVGYVDTAKGMLPDKNVHIFVSMIAQSVTAAGLLSYPTVRRMM 239
DB 181 VGGIIYRAAFVGYVDTAKGMLPDKNVHIFVSMIAQSVTAAGLLSYPTVRRMM 240
QY 240 QSGRKGADIMYTGVDCKRKIADEGAKAFPKGAMSVNLKMGCAFVLVYDELKCV 297
DB 241 QSGRKGADIMYTGVDCKRKIFRDEGKAFPKGAMSVNLKMGCAFVLVYDELKCV 298

RESULT 9

US-09-185-904A-33
Sequence 33, Application US/09185904A
Patent No. US20020177185A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Willey, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 660088.420
CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-185-904A-33

Query Match 89.2%; Score 1385.5; DB 10; Length 298;
Best Local Similarity 87.2%; Pred. No. 3.7e-142;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYGIIDCVR 60
DB 1 MTEQALSPKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYGIIDCVR 60
QY 61 IPKEGGLSPFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDHKKQFWRYPAGNLASG 120
DB 61 IPKEGGLSPFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDHKKQFWRYPAGNLASG 120
QY 121 GAAGATSLCFVYPLDPARTRLAADVGR-AGREFHGLDCCIIFKSDGLRGLYQGFVS 179
DB 121 GAAGATSLCFVYPLDPARTRLAADVGR-AGREFHGLDCCIIFKSDGLRGLYQGFVS 180
QY 180 VGGIIYRAAFVGYVDTAKGMLPDKNVHIFVSMIAQSVTAAGLLSYPTVRRMM 239
DB 180 VGGIIYRAAFVGYVDTAKGMLPDKNVHIFVSMIAQSVTAAGLLSYPTVRRMM 240
QY 240 QSGRKGADIMYTGVDCKRKIADEGAKAFPKGAMSVNLKMGCAFVLVYDELKCV 297
DB 241 QSGRKGADIMYTGVDCKRKIFRDEGKAFPKGAMSVNLKMGCAFVLVYDELKCV 298

RESULT 10

US-10-029-386-32501
Sequence 32501, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: ABOMICA-X-2

```

; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32501
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004000.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.95
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96
; OTHER INFORMATION: SWISSPROT HIT: P05141, EVALU2 2.00e-83
US-10-029-386-32501

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Query Match      49.8%; Score 773.5; DB 12; Length 179;
Best Local Similarity 88.3%; Pred. No. 6.7e-76;
Matches 144; Conservative 12; Mismatches 6; Indels 1; Gaps 1;

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QY 38 VQHASQKQISAKQYKGIIDCVRIPEKQGLSPFMRGNLANYRYPTQALNPAFKQYKQ 97
DB 1 VQHASQKQITADKQYKGIIDCVRIPEKQGLSPFMRGNLANYRYPTQALNPAFKQYKQ 60
QY 98 LFLGVDRHKQFWRFPAGNLASGGAAGATSLCFVYPLDPAFTRLAADVGR--AQREPHGL 156
DB 61 IFLGVDRKRTQFWLTFANLBSGGAGATSLCFVYPLDPAFTRLAADVGRKGAERFRGL 120
QY 157 GDCIILKIFKSDGLNGLYOGFNVSVQGIITRYAAYGVYDTAKG 199
DB 121 GDCIIVKIYKSDGIRKGLYOGFNVSVQGIITRYAAYGVYDTAKG 163

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RESULT 11
US-10-032-585-7194
; Sequence 7194, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jlang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OR INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7194
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-032-585-7194

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```

Query Match      49.6%; Score 771; DB 12; Length 301;
Best Local Similarity 53.9%; Pred. No. 2.5e-75;
Matches 158; Conservative 43; Mismatches 82; Indels 10; Gaps 5;

```

```

QY 7 SFLKDFLAGAANAASKTAAVPIERVKLLIOVQ--HASQKQISAKQYKGIIDCVRIPEKQ 65
DB 5 NFPLDPLMGVSAVSTAAPIERVKLLIOVQ--DEMIKAGRLSEBYKIGDCEFRITK 64
QY 66 GFLSPFMRGNLANYRYPTQALNPAFKQYKQGLFQVDRHKQFWRFPAGNLASGGA 125
DB 65 GVSFMRGNLANYRYPTQALNPAFKQYKQGLFQVDRHKQFWRFPAGNLASGGA 122
QY 126 TSLGCVYPLDPAFTRLAADVGR--AQREPHGLDGLNGLYOGFNVSVQGIITRYAAYGVYDTAKG 182
DB 123 TSLGCVYPLDPAFTRLAADVGR--AQREPHGLDGLNGLYOGFNVSVQGIITRYAAYGVYDTAKG 182
QY 183 IITRYAAYGVYDTAKG--MLPDPKVVHIFVSMMLAQSTAVAGLLSYFPDTRRRMMMQS 241

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DB 183 IIVYRGALYFGLYDLSKPLVVLGPIEGSFLASFLFGMAVTTGASLASYPLDTRRRMMMQS 242
QY 242 GRKADIMTYGTVDCKRIADGAKAFPFKAGMSNVIRKMGAGAVLYLYDEIK 294
DB 243 GQA---VYTDGALDPCFRKVAABGVSLFKCGGANILRGVAGAVISLYDQLQ 292

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RESULT 12
US-10-141-478A-2
; Sequence 2, Application US/10141478A
; Publication No. US20030148300A1
; GENERAL INFORMATION:
; APPLICANT: Valentin, Henry
; APPLICANT: Savage, Thomas
; APPLICANT: Voelker, Toni
; APPLICANT: Zang, Wei
; TITLE OR INVENTION: Metabolite Transporters
; FILE REFERENCE: 16515.146
; CURRENT APPLICATION NUMBER: US/10/141,478A
; CURRENT FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: US 60/289,519
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 60/289,527
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: To Be Assigned, Attorney Docket No. US20030148300A1: 16517.
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-141-478A-2

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Query Match      47.6%; Score 740; DB 12; Length 381;
Best Local Similarity 53.6%; Pred. No. 8.1e-72;
Matches 165; Conservative 39; Mismatches 76; Indels 28; Gaps 8;

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```

QY 7 SFLKDFLAGAANAASKTAAVPIERVKLLIOVQHASQKQISA--EKQYKGIIDCVRIPEK 63
DB 79 NFALDPLMGVSAVSTAAPIERVKLLIOVQ--DEMIKAGRLSEBYKIGDCEFRITK 136
QY 64 GFLSPFMRGNLANYRYPTQALNPAFKQYKQGLFQVDRHKQFWRFPAGNLASGGA 123
DB 137 DEFGSLMRGNLANYRYPTQALNPAFKQYKQGLFQVDRHKQFWRFPAGNLASGGA 195
QY 124 GATSLCFVYPLDPAFTRLAADVGRBAO---RPFHGLDGLNGLYOGFNVSVQGIITRYAAYGVYDTAKG 179
DB 196 GASLFLVYSLDPAFTRLAADVGRBAO---RPFHGLDGLNGLYOGFNVSVQGIITRYAAYGVYDTAKG 255
QY 180 VQGIITRYAAYGVYDTAKG---GMLPDPKVVHIFVSMMLAQSTAVAGLLSYFPDTR 234
DB 256 CVGIIVYRGALYFGLYDLSKPLVVLGPIEGSFLASFLFGMAVTTGASLASYPLDTRRRMMMQS 311
QY 235 RRMMSGGRKADIMTYGTVDCKRIADGAKAFPFKAGMSNVIRKMGAGAVLYLYDEIK 293
DB 312 RRMMSGGRKADIMTYGTVDCKRIADGAKAFPFKAGMSNVIRKMGAGAVLYLYDEIK 293
QY 294 -----KKY 296
DB 369 LTVRGKTY 376

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RESULT 13
US-09-801-368-252
; Sequence 252, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug

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; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Sumner, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: Patent version 3.0
; SEQ ID NO: 252
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; US-09-801-368-252

Query Match          47.3%; Score 734; DB 10; Length 318;
Best Local Similarity 53.2%; Pred. No. 2.8e-71;
Matches 156; Conservative 45; Mismatches 82; Indels 10; Gaps 5;

OY 7 SFLDPLAGAAVAAVSKTAVAPIRERVKLLQVO-HASQISAEKQYKGIIDCVIRPEQ 65
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 22 NFLIDFLMGVSAVAAKTAAASPIERVKLLIQNDMLKQGLTRKTAAGILDDFKKTATQ 81
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 66 GFLSFRGNLANVIRYPTQALNPAFKQYKQLFSGVDHRKQFWRYPFAGNLASGAAGA 125
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 82 GVISTWRGNTANVIRYPTQALNPAFKQYKQIMF--GRKGGVAKWRPAGNLASGAAGA 139
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 126 TSLCFVYPLDPARTRLAAD--VGRARQEPHGLDCCIIRKIPKSDGLRGLYOGFNVSV 182
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 140 LSLFVYSLDVARTRRLAADSCKSGKGAQFNGLLIDVYKKTLSGDAVGLYRGLPSTVVG 199
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 183 IIVYAAAFRGVYDTAKGMLPDPKXVHIFV-SWMIAQSVAVAGLISYPPDTRRRMMQ 241
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 200 IVVYGLYFGVMDSLKPLLLTGLSGFLASFLGQVAVVTGASTCSYPLDTRRRMMQ 259
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 242 GRKGAIDIMYTVDCWRKTIADKGAAPFKGAMSVNLRGMGAFVLYLDEIK 294
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 260 GQA---VKYDGAFLDKRKIVAAEGVGLFKGCGANILRGVAGAGVISMVDQLQ 309
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
US-09-734-569-170
; Sequence 170, Application US/09734569
; Patent No. US20020064816A1
; GENERAL INFORMATION:
; APPLICANT: Lerchl, Jens
; APPLICANT: Renz, Andreas
; APPLICANT: Ehrhardt, Thomas
; APPLICANT: Reinold, Andreas
; APPLICANT: Cirus, Petra
; APPLICANT: Bischoff, Friedrich
; APPLICANT: Frank, Markus
; APPLICANT: Freund, Annette
; APPLICANT: Duwenig, Elke
; APPLICANT: Schmidt, Ralf-Michael
; APPLICANT: Reeki, Ralf
; TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved
; FILE REFERENCE: BASF-NAE-1332-99-US
; CURRENT APPLICATION NUMBER: US/09/734,569
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/171,101
; PRIOR FILING DATE: 1999-12-16
```

```

; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: Patent Ver. 2.1/WordPerfect 6.1
; SEQ ID NO: 170
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Physcomitrella patens
; US-09-734-569-170

Query Match          47.3%; Score 734; DB 9; Length 386;
Best Local Similarity 52.9%; Pred. No. 3.7e-71;
Matches 156; Conservative 43; Mismatches 84; Indels 12; Gaps 6;

OY 7 SFLDPLAGAAVAAVSKTAVAPIRERVKLLQVO-HASQISAEKQYKGIIDCVIRPEQ 65
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 84 SFTMDFLMGVSAVAVSKTAAPIRERVKLLIQNDMLKQGLSHRYPKIGICFSTVDO 143
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 66 GFLSFRGNLANVIRYPTQALNPAFKQYKQLFSGVDHRKQ-FWRYPAGNLASGAAG 124
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 144 GMSLWRGNTANVIRYPTQALNPAFKDYFSLF--GYKKQDQGWKWFAGNLASGAAG 201
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 125 ATSLCFVYPLDPARTRLAADYGR--AQRHFGHGLDCCIIRKIPKSDGLRGLYOGFNVSV 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 202 ASLFLFVYSLDVARTRRLAADSCKSGKGERQFNGLLIDVYKKTATDGIAGLYRGLAIS 261
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 181 OGIIIVYAAAFRGVYDTAKG-MLPDPKXVHIFV-SWMIAQSVAVAGLISYPPDTRRRMM 239
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 262 AGIIVYRLYGLYDLSLPPVAVNLBNFLASFLGNGITGAGLASYPIDTVRRMM 321
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 240 QSRGKGAIDIMYTVDCWRKTIADKGAAPFKGAMSVNLRGMGAFVLYLDEIK 294
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 322 TSGRA---VKYNGSMDAPKQILAKGAKSLFKGAGANILRGVAGAGVLSGVDQLQ 373
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
US-10-128-714-3338
; Sequence 3338, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wengli
; APPLICANT: Tienkoef, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Broghkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: Patent version 3.1
; SEQ ID NO: 3338
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
; US-10-128-714-3338

Query Match          45.3%; Score 703.5; DB 15; Length 308;
Best Local Similarity 50.8%; Pred. No. 5.7e-68;
Matches 150; Conservative 45; Mismatches 87; Indels 13; Gaps 6;

OY 7 SFLDPLAGAAVAAVSKTAVAPIRERVKLLQVOHASQISA--EKQYKGIIDCVIRIPK 63
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```



```

Db      7 APTDSFAVGVSAASVSKTAAPIERIKL--VQNDQMIRAGRLDRKTYNGIIDCFRTAQ 64
Qy      64 EOGPLSFMRGNLANYIRYPTQALNFAFKDKYKOLFQGVDRHQFMRYPAGNLASGGA 123
Db      65 AEGVMSLWRGNANVIRYPTQALNFAFRDITYKSMFAYKKDR-DGYAKMMGNLASGGA 123
Qy      124 GATSLCFYYPPLDFARTRLAADVGR--AOREFHGLADCIIFKSDGLRGLYOGFNVS 180
Db      124 GATSLCFYYPPLDFARTRLAADVGR--AOREFHGLADCIIFKSDGLRGLYOGFNVS 180
Qy      124 GATSLCFYYPPLDFARTRLAADVGR--AOREFHGLADCIIFKSDGLRGLYOGFNVS 180
Db      124 GATSLCFYYPPLDFARTRLAADVGR--AOREFHGLADCIIFKSDGLRGLYOGFNVS 180
Qy      181 OGIIITYRAAYFGVDTAKG-MLPDPKNVHIFVSMNIAQSVTAAGLSYPFDVRRMM 239
Db      184 LGIVVYRGLYFGMYDSIRPVVYVCSLEGSFLASFLIGWTVTGAGIASYPLDTIRRRMM 243
Qy      240 OSGRRGADIMYTGDCWRKXAKDEGAKAFPKGMSNVLRGMGAFVLYDEIK 294
Db      244 TSGER--VKTKSSIDAARQIIRAKGVKSLFKGAGANILRGVAGVLSITYDQV 295

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Search completed: December 18, 2003, 12:55:43
 Job time : 25.278 secs

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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:37:46 ; Search time 14.3012 Seconds
(without alignments)
1997.178 Million cell updates/sec

Title: US-09-811-131-31

Perfect score: 1553

Sequence: 1 MGDHMSFLNDPLAAGAVAA.....LRGNGAFVLVDEIKKYV 297

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308 ,

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1526.5	98.3	298	1 A44778	ADP,ATP carrier pr
2	1466.5	94.4	298	2 160173	adenine nucleotide
3	1463.5	94.2	298	3 S37210	ADP,ATP carrier pr
4	1458.5	93.9	298	1 XMBO	ADP,ATP carrier pr
5	1391.5	89.6	298	1 A29132	ADP,ATP carrier pr
6	1385.5	89.2	298	1 S03894	ADP,ATP carrier pr
7	1380.5	88.9	298	2 B33646	ADP,ATP carrier pr
8	1368.5	88.1	298	2 S31814	ADP,ATP carrier pr
9	1142.5	73.6	301	1 S31935	ADP,ATP carrier pr
10	1045.5	67.3	313	2 T25850	ADP,ATP carrier pr
11	1043.5	67.2	313	2 T23207	ADP,ATP carrier pr
12	1037.5	66.8	300	2 T25371	ADP,ATP carrier pr
13	1005.5	64.7	300	2 T15206	ADP,ATP carrier pr
14	973.5	62.7	339	2 A41677	ADP,ATP carrier pr
15	904.5	58.2	301	2 S51132	ADP,ATP carrier pr
16	772	49.7	306	2 T20012	ADP,ATP carrier pr
17	770.5	49.6	308	1 S30259	ADP,ATP carrier pr
18	756.5	48.7	322	2 T40526	ADP,ATP carrier pr
19	752.5	48.5	322	2 T40526	ADP,ATP carrier pr
20	752.5	48.5	322	2 T40526	ADP,ATP carrier pr
21	751.5	48.4	387	2 S16568	ADP,ATP carrier pr
22	746.5	48.1	379	2 T04608	ADP,ATP carrier pr
23	746.5	48.1	382	2 S33630	ADP,ATP carrier pr
24	745.5	48.0	326	2 T25728	ADP,ATP carrier pr
25	745.5	48.0	386	2 S17917	ADP,ATP carrier pr
26	744.5	47.9	386	2 S17917	ADP,ATP carrier pr
27	740	47.6	379	2 S21313	ADP,ATP carrier pr
28	740	47.6	386	2 S14874	ADP,ATP carrier pr
29	737	47.5	385	1 S29852	ADP,ATP carrier pr

30	736	47.4	307	2 A36582	ADP,ATP carrier pr
31	734	47.3	318	1 A31978	ADP,ATP carrier pr
32	733.5	47.2	313	1 XMNC	ADP,ATP carrier pr
33	729	46.9	303	2 S68154	ADP,ATP carrier pr
34	728.5	46.9	306	2 T42011	ADP,ATP carrier pr
35	718.5	46.3	309	2 A24849	ADP,ATP carrier pr
36	676	43.5	298	2 T24029	ADP,ATP carrier pr
37	508	32.7	327	2 T51577	ADP,ATP carrier pr
38	368	23.7	415	2 T48171	ADP,ATP carrier pr
39	367.5	23.7	325	2 T04273	ADP,ATP carrier pr
40	363	23.4	381	2 T51158	ADP,ATP carrier pr
41	350.5	22.6	475	2 T50686	ADP,ATP carrier pr
42	349.5	22.5	352	2 T01729	ADP,ATP carrier pr
43	345.5	22.2	358	2 T45934	ADP,ATP carrier pr
44	334.5	21.5	348	2 D84798	ADP,ATP carrier pr
45	327	21.1	332	2 T47703	ADP,ATP carrier pr

ALIGNMENTS

RESULT 1
A44778
ADP,ATP carrier protein T1 - human
N:Alternate names: mitochondrial ADP,ATP translocase 1
C:Species: Homo sapiens (man)
C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C:Accession: A44778, S03893, A39891, A28116
R:Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, M.
J. Biol. Chem. 264, 13998-14004, 1989
A:Title: A human muscle adenine nucleotide translocator gene has four exons, is located
A:Reference number: A44778, MUID:89340499; PMID:2547778
A:Accession: A44778
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-298 <L1A>
A:Cross-references: GB:004982; NID:g178658; PIDN:AAA51736.1; PID:g178659
R:Cooren, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A:Title: DNA sequence of two expressed nuclear genes for human mitochondrial ADP/ATP tr.
A:Reference number: S03893; MUID:89236396; PMID:2541251
A:Accession: S03893
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-298 <CO2>
R:Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.
Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987
A:Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader
A:Reference number: A39891, MUID:86041149; PMID:2823266
A:Accession: A39891
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15, 'A', 17-146, 'RR', 149, 151-226, 'L', 228-298 <NEC>
A:Cross-references: GB:002966; NID:g339919; PIDN:AAA61223.1; PID:g339920
R:Experimental source: clone pEMANT
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a
A:Reference number: A94197, MUID:88124845; PMID:2829183
A:Accession: A28116
A:Molecule type: mRNA
A:Residues: 1-37 <HOU>
A:Cross-references: GB:003993; NID:g339724; PIDN:AAA6751.1; PID:g339725
A:Experimental source: liver
C:Genetics:
A:Gene: GDB:ANT1, T1
A:Cross-references: GDB:119680; OMIM:103220
A:Map position: 4q35-4q35
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; homodimer; mitochondrial; transmembrane protein
F:2-298/Protein: ADP,ATP carrier protein #status predicted <MAT>
F:5-99/DNA: ADP,ATP carrier protein repeat homology <ACPI>
F:110-202/DNA: ADP,ATP carrier protein repeat homology <ACP2>

F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 98.3%; Score 1526.5; DB 1; Length 298;
Best Local Similarity 98.3%; Pred. No. 1.5e-130;
Matches 293; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 MGDHMSFLKDFLAGAANAASKTAVADIERVKLLQVQHASKOISAEKQYKGIIDCVR 60
Db 1 MGDHMSFLKDFLAGAANAASKTAVADIERVKLLQVQHASKOISAEKQYKGIIDCVR 60
Qy 1 IPKQGFSLFMRGNLANVIRFPQALNPAFKDKYKQFLGSDVRHQPFWYFPGNLASG 120
Db 1 IPKQGFSLFMRGNLANVIRFPQALNPAFKDKYKQFLGSDVRHQPFWYFPGNLASG 120
Qy 121 GAAGATSLCFYYPIDFARTRLAADVGR-RAQREPHGLDCCIIFKSDGLRGLYQGFNV 179
Db 121 GAAGATSLCFYYPIDFARTRLAADVGR-RAQREPHGLDCCIIFKSDGLRGLYQGFNV 180
Qy 180 VQGIITIRAAVFGYVDTAKGMLPDPKXVHIFVSMWIAQSVTAVALVSPDYRRRRMM 239
Db 180 VQGIITIRAAVFGYVDTAKGMLPDPKXVHIFVSMWIAQSVTAVALVSPDYRRRRMM 240
Qy 240 QSGRKGADIMTGTVDCKRKIAKDEGAKAFPGKAMSNVLRGMGAFVLVYDEIKKY 297
Db 241 QSGRKGADIMTGTVDCKRKIAKDEGAKAFPGKAMSNVLRGMGAFVLVYDEIKKY 298

RESULT 2

160173 adenine nucleotide translocator - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999

C;Accession: 160173

R;Shinohara, Y.; Kamida, M.; Yamazaki, N.; Terada, H.

Biochim. Biophys. Acta 1152, 192-196, 1993

A;Title: Isolation and characterization of cDNA clones and a genomic clone encoding rat

A;Reference number: 160173; MUID:94002161; PMID:8399300

A;Accession: 160173

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-298 <RES>

A;Cross-references: EMBL:X61667; NID:g400426; PIDN:CAA3842.1; PID:g400427

C;Genetics:

A;Gene: ancl

A;Intons: 37/3; 200/1; 247/1

C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C;Keywords: duplication; transmembrane protein

F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 94.4%; Score 1466.5; DB 2; Length 298;
Best Local Similarity 94.4%; Pred. No. 4.1e-125;
Matches 281; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

Qy 1 MGDHMSFLKDFLAGAANAASKTAVADIERVKLLQVQHASKOISAEKQYKGIIDCVR 60
Db 1 MGDHMSFLKDFLAGAANAASKTAVADIERVKLLQVQHASKOISAEKQYKGIIDCVR 60
Qy 61 IPKQGFSLFMRGNLANVIRFPQALNPAFKDKYKQFLGSDVRHQPFWYFPGNLASG 120
Db 61 IPKQGFSLFMRGNLANVIRFPQALNPAFKDKYKQFLGSDVRHQPFWYFPGNLASG 120
Qy 121 GAAGATSLCFYYPIDFARTRLAADVGR-RAQREPHGLDCCIIFKSDGLRGLYQGFNV 179
Db 121 GAAGATSLCFYYPIDFARTRLAADVGR-RAQREPHGLDCCIIFKSDGLRGLYQGFNV 180
Qy 180 VQGIITIRAAVFGYVDTAKGMLPDPKXVHIFVSMWIAQSVTAVALVSPDYRRRRMM 239
Db 180 VQGIITIRAAVFGYVDTAKGMLPDPKXVHIFVSMWIAQSVTAVALVSPDYRRRRMM 240
Qy 240 QSGRKGADIMTGTVDCKRKIAKDEGAKAFPGKAMSNVLRGMGAFVLVYDEIKKY 297
Db 241 QSGRKGADIMTGTVDCKRKIAKDEGAKAFPGKAMSNVLRGMGAFVLVYDEIKKY 298

Db 241 QSGRKGADIMTGTVDCKRKIAKDEGAKAFPGKAMSNVLRGMGAFVLVYDEIKKY 298

RESULT 3

S37210

ADP,ATP carrier protein T1 - mouse

N;Alternate names: adenine nucleotide carrier

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999

C;Accession: S37210

R;Laplace, C.; Coate, P. submitted to the EMBL data library, September 1993

A;Reference number: S37210

A;Accession: S37210

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-298 <LAP>

A;Cross-references: EMBL:X74510; NID:g402627; PIDN:CAA52616.1; PID:g402628

C;Genetics:

A;Gene: Ancl

C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C;Keywords: duplication; transmembrane protein

F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 94.2%; Score 1463.5; DB 2; Length 298;
Best Local Similarity 94.0%; Pred. No. 7.6e-125;
Matches 280; Conservative 10; Mismatches 7; Indels 1; Gaps 1;

Qy 1 MGDHMSFLKDFLAGAANAASKTAVADIERVKLLQVQHASKOISAEKQYKGIIDCVR 60
Db 1 MGDHMSFLKDFLAGAANAASKTAVADIERVKLLQVQHASKOISAEKQYKGIIDCVR 60
Qy 61 IPKQGFSLFMRGNLANVIRFPQALNPAFKDKYKQFLGSDVRHQPFWYFPGNLASG 120
Db 61 IPKQGFSLFMRGNLANVIRFPQALNPAFKDKYKQFLGSDVRHQPFWYFPGNLASG 120
Qy 121 GAAGATSLCFYYPIDFARTRLAADVGR-RAQREPHGLDCCIIFKSDGLRGLYQGFNV 179
Db 121 GAAGATSLCFYYPIDFARTRLAADVGR-RAQREPHGLDCCIIFKSDGLRGLYQGFNV 180
Qy 180 VQGIITIRAAVFGYVDTAKGMLPDPKXVHIFVSMWIAQSVTAVALVSPDYRRRRMM 239
Db 180 VQGIITIRAAVFGYVDTAKGMLPDPKXVHIFVSMWIAQSVTAVALVSPDYRRRRMM 240
Qy 240 QSGRKGADIMTGTVDCKRKIAKDEGAKAFPGKAMSNVLRGMGAFVLVYDEIKKY 297
Db 241 QSGRKGADIMTGTVDCKRKIAKDEGAKAFPGKAMSNVLRGMGAFVLVYDEIKKY 298

RESULT 4

XWBO

ADP,ATP carrier protein T1 - bovine

N;Alternate names: ADP/ATP translocase T1

C;Species: Bos primigenius taurus (cattle)

C;Date: 14-Nov-1993 #sequence_revision 22-Jul-1994 #text_change 22-Jun-1999

C;Accession: A43646; A24822; A03181; A61343; S69369

R;Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E. Biochemistry 28, 866-873, 1989

A;Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in

A;Reference number: A43646; MUID:99229093; PMID:2540808

A;Accession: A43646

A;Molecule type: mRNA

A;Residues: 1-298 <POW>

A;Cross-references: GB:A24102; NID:g529414; PIDN:AAA30768.1; PID:g529415

R;Raamussen, U.B.; Mohlrad, H. Biochem. Biophys. Res. Commun. 139, 850-857, 1986

A;Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unusual

A;Reference number: A24822; MUID:86295775; PMID:3017341

A;Accession: A24822

A;Molecule type: mRNA

A;Residues: 208-298 <RAS>

A/Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1; PID:g162631
 R:Aquila, H.; Misa, D.; Eulitz, M.; Klingenberg, M.
 Hope-Sevler's Z. Physiol. Chem. 363, 345-349, 1982
 A/Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondria
 A/Reference number: A03181; MUID:82188267; PMID:7076130
 A/Accession: A03181
 A/Molecule type: protein
 A/Residues: 2-51, 'X', '53-70', 'X', '72-109', 'X', '111-238' <ANU>
 A/Note: residue 52 may be methyllysine
 R:Beckel, W.; Wachter, E.; Aquila, H.; Klingenberg, M.
 Biochim. Biophys. Acta 670, 176-180, 1981
 A/Title: Amino acid sequence determination of the ADP/ATP carrier from beef heart mitochondria
 A/Reference number: A61343; MUID:82046808; PMID:6271240
 A/Accession: A61343
 A/Molecule type: protein
 A/Residues: 205-238 <BAB>
 R:Oetmeier, W.; Masson, K.; Kalina, S.
 Eur. J. Biochem. 227, 730-733, 1995
 A/Title: [(3)H]-2,4-dichloro-4-isopropylacridone labels Cys159 of the bovine mitochondrial ADP/ATP carrier
 A/Reference number: S69369; MUID:95172058; PMID:7867632
 A/Accession: S69369
 A/Molecule type: protein
 A/Residues: 49-63;154-168 <OET>
 C/Comment: This protein is synthesized in the cytosol and transported into the mitochondria
 C/Complex: homodimer
 C/Function:
 A/Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP generated by oxidative phosphorylation in the inner mitochondrial membrane
 A/Note: located in the inner mitochondrial membrane
 C/Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C/Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mitochondria
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACPI>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>
 F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
 F:52/Modified site: N6-methyllysine (Lys) #status predicted

Query Match 93.9%; Score 1458.5; DB 1; Length 298;
 Best Local Similarity 94.3%; Pred. No. 2.2e-114;
 Matches 281; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAAGAAVSKTAVAPIRVKKLLQVQHSKQISAEKQYKGIIDCVR 60
 DB 1 MSDQALSLKDFLAGAAGAAVSKTAVAPIRVKKLLQVQHSKQISAEKQYKGIIDCVR 60

QY 61 IPKQGLSTFRKGLAVIRFPQALNPAKPKYKQLFLGVDNRHQPFMYFFAGNTASG 120
 DB 61 IPKQGLSTFRKGLAVIRFPQALNPAKPKYKQLFLGVDNRHQPFMYFFAGNTASG 120

QY 121 GAAGATSLCFYVPLDPAFRTLRADVGR-RAQREPHGAGDCIIRKFKSDGRLGLVQGFNV 179
 DB 121 GAAGATSLCFYVPLDPAFRTLRADVGR-RAQREPHGAGDCIIRKFKSDGRLGLVQGFNV 179

QY 180 VQGIIRYRAAYFGVYDPAKGLPDPKXVHIFVSMIAQSVYAVAGLSYFDPYRRMM 239
 DB 180 VQGIIRYRAAYFGVYDPAKGLPDPKXVHIFVSMIAQSVYAVAGLSYFDPYRRMM 239

QY 240 QSGRKADIMYTGVDWCRIKADDEKAKAFKGMASVNLKMGAFVLYDEIKKY 297
 DB 240 QSGRKADIMYTGVDWCRIKADDEKAKAFKGMASVNLKMGAFVLYDEIKKY 297

QY 241 QSGRKADIMYTGVDWCRIKADDEKAKAFKGMASVNLKMGAFVLYDEIKKY 298
 DB 241 QSGRKADIMYTGVDWCRIKADDEKAKAFKGMASVNLKMGAFVLYDEIKKY 298

RESULT 5
 A29132
 ADP/ATP carrier protein T2 - human
 N/Alternate names: mitochondrial ADP/ATP translocase 2
 C/Species: Homo sapiens (man)
 C/Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
 C/Accession: A29132; C28116
 R:Beckel, W.; Wachter, E.; Aquila, H.; Klingenberg, M.
 J. Biol. Chem. 262, 4355-4359, 1987
 A/Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulated
 A/Reference number: A29132; MUID:8716056; PMID:3031073
 A/Accession: A29132

A/Molecule type: mRNA
 A/Residues: 1-298 <BAT>
 A/Cross-references: GB:002683; NID:g179246; PIDN:AAA35579.1; PID:g179247
 R:Houldsworth, J.; Attardi, G.
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
 A/Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a
 A/Reference number: A94197; MUID:88124845; PMID:2829183
 A/Accession: C28116
 A/Molecule type: mRNA
 A/Residues: 47-65, 'G', 67-110, 'U', 112-161, 'G', 163-298 <HOU>
 A/Cross-references: GB:003591; NID:g339720; PIDN:AAA36749.1; PID:g339721
 A/Experimental source: clone pBAT3
 C/Genetics:
 A/Gene: GDB:AMT2; T3; 2P1
 A/Cross-references: GDB:125190; OMIM:300150
 A/Map position: Xq13-Xq26
 A/Note: there may be some confusion in the assignment of sequences for GDB:AMT2 and GDB:
 C/Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C/Keywords: duplication; homodimer; mitochondria; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACPI>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 89.6%; Score 1391.5; DB 1; Length 298;
 Best Local Similarity 88.6%; Pred. No. 2.5e-118;
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAAGAAVSKTAVAPIRVKKLLQVQHSKQISAEKQYKGIIDCVR 60
 DB 1 MTDQALSLKDFLAGAAGAAVSKTAVAPIRVKKLLQVQHSKQISAEKQYKGIIDCVR 60

QY 61 IPKQGLSTFRKGLAVIRFPQALNPAKPKYKQLFLGVDNRHQPFMYFFAGNTASG 120
 DB 61 IPKQGLSTFRKGLAVIRFPQALNPAKPKYKQLFLGVDNRHQPFMYFFAGNTASG 120

QY 121 GAAGATSLCFYVPLDPAFRTLRADVGR-RAQREPHGAGDCIIRKFKSDGRLGLVQGFNV 179
 DB 121 GAAGATSLCFYVPLDPAFRTLRADVGR-RAQREPHGAGDCIIRKFKSDGRLGLVQGFNV 179

QY 180 VQGIIRYRAAYFGVYDPAKGLPDPKXVHIFVSMIAQSVYAVAGLSYFDPYRRMM 239
 DB 180 VQGIIRYRAAYFGVYDPAKGLPDPKXVHIFVSMIAQSVYAVAGLSYFDPYRRMM 239

QY 240 QSGRKADIMYTGVDWCRIKADDEKAKAFKGMASVNLKMGAFVLYDEIKKY 296
 DB 240 QSGRKADIMYTGVDWCRIKADDEKAKAFKGMASVNLKMGAFVLYDEIKKY 296

QY 241 QSGRKADIMYTGVDWCRIKADDEKAKAFKGMASVNLKMGAFVLYDEIKKY 297
 DB 241 QSGRKADIMYTGVDWCRIKADDEKAKAFKGMASVNLKMGAFVLYDEIKKY 297

RESULT 6
 S03894
 ADP/ATP carrier protein T3 - human
 N/Alternate names: ADP/ATP carrier protein T2 (misidentification); mitochondrial ADP/ATP
 C/Species: Homo sapiens (man)
 C/Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
 C/Accession: S03894; B28116
 R:Cozens, A.L.; Rumbold, M.J.; Walker, J.E.
 J. Mol. Biol. 206, 261-280, 1989
 A/Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr.
 A/Reference number: S03893; MUID:89236396; PMID:2541251
 A/Accession: S03894
 A/Status: not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 1-298 <COZ>
 R:Houldsworth, J.; Attardi, G.
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
 A/Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a
 A/Reference number: A94197; MUID:88124845; PMID:2829183
 A/Accession: B28116
 A/Molecule type: mRNA
 A/Residues: 36-104, 'R', 106, 'A', 109-298 <HOU>
 A/Cross-references: GB:003592; NID:g339722; PIDN:AAA36750.1; PID:g339723
 A/Experimental source: liver
 C/Genetics:

A;Gene: GDB:ANT3; ANT3Y
A;Cross-references: GDB:125184; OMIM:300151; OMIM:403000
A;Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
A;Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and GDB:
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F;2-298/Product: ADP,ATP carrier protein status predicted <MAT>
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 89.2%; Score 1385.5; DB 1; Length 298;
Best Local Similarity 87.2%; Pred. No. 8.8e-118;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHAFSLKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYGIIDCVR 60
DB 1 MTEQALSFADPFLAGIAAISKTAAPIERVKLLQVQHASKOISAEKQYGIIDCVR 60
QY 61 IPKEQGLSPWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHQPFRYFAGNLASG 120
DB 61 IPKEQGLSPWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHQPFRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFAFRTLAADVGR-AGREPHGLGDCIYIKFKSDGLRGLYQGFNV 179
DB 121 GAAGATSLCFVYPLDFAFRTLAADVGR-AGREPHGLGDCIYIKFKSDGLRGLYQGFNV 180
QY 180 VQGIITIRAAVFGYVDPAKAGLPPDKNVHIFVSMIAQSVTAVALGLSYPPDYRRMM 239
DB 181 VQGIITIRAAVFGYVDPAKAGLPPDKNVHIFVSMIAQSVTAVALGLSYPPDYRRMM 240
QY 240 QSGRKGADIMYTGVDGCRKIADDEGAKAFKGMNSVLRMGGAFLVLYDEIKKY 297
DB 241 QSGRKGADIMYTGVDGCRKIFRDEGKAFKGMNSVLRMGGAFLVLYDEIKKY 298

RESULT 7

B43646
ADP,ATP carrier protein T2 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999
C;Accession: B43646
R;Powell, S.U.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
Biochemistry 28, 866-873, 1989
A;Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
A;Reference number: A43646; PMID:89229093; PMID:2540808
A;Accession: B43646
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-298 <POM>
A;Cross-references: GB:M24103; NID:G529416; PIDN:AAA30769.1; PID:G529417
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 88.9%; Score 1380.5; DB 2; Length 298;
Best Local Similarity 86.9%; Pred. No. 2.5e-117;
Matches 259; Conservative 21; Mismatches 17; Indels 1; Gaps 1;
QY 1 MGDHAFSLKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYGIIDCVR 60
DB 1 MTEQALSFADPFLAGIAAISKTAAPIERVKLLQVQHASKOISAEKQYGIIDCVR 60
QY 61 IPKEQGLSPWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHQPFRYFAGNLASG 120
DB 61 IPKEQGLSPWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHQPFRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFAFRTLAADVGR-AGREPHGLGDCIYIKFKSDGLRGLYQGFNV 179
DB 121 GAAGATSLCFVYPLDFAFRTLAADVGR-AGREPHGLGDCIYIKFKSDGLRGLYQGFNV 180

QY 180 VQGIITIRAAVFGYVDPAKAGLPPDKNVHIFVSMIAQSVTAVALGLSYPPDYRRMM 239
DB 181 VQGIITIRAAVFGYVDPAKAGLPPDKNVHIFVSMIAQSVTAVALGLSYPPDYRRMM 240
QY 240 QSGRKGADIMYTGVDGCRKIADDEGAKAFKGMNSVLRMGGAFLVLYDEIKKY 297
DB 241 QSGRKGADIMYTGVDGCRKILDEGAKAFKGMNSVLRMGGAFLVLYDEIKKY 298

RESULT 8

S31814
ADP,ATP carrier protein T2 - mouse
N;Alternate names: adenine nucleotide translocase
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Apr-1998
C;Accession: S31814
R;Costet, P.; Laplace, C.
submitted to the EMBL data library, January 1993
A;Reference number: S31814
A;Accession: S31814
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-298 <COS>
A;Cross-references: EMBL:X70847
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: duplication; transmembrane protein
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 88.1%; Score 1368.5; DB 2; Length 298;
Best Local Similarity 87.2%; Pred. No. 3e-116;
Matches 259; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

QY 1 MGDHAFSLKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYGIIDCVR 60
DB 1 MTDNAVSFADPFLAGIAAISKTAAPIERVKLLQVQNDRTTADQYKGIIDCVR 60
QY 61 IPKEQGLSPWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHQPFRYFAGNLASG 120
DB 61 IPKEQGLSPWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHQPFRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFAFRTLAADVGR-AGREPHGLGDCIYIKFKSDGLRGLYQGFNV 179
DB 121 GAAGATSLCFVYPLDFAFRTLAADVGR-AGREPHGLGDCIYIKFKSDGLRGLYQGFNV 180
QY 180 VQGIITIRAAVFGYVDPAKAGLPPDKNVHIFVSMIAQSVTAVALGLSYPPDYRRMM 239
DB 181 VQGIITIRAAVFGYVDPAKAGLPPDKNVHIFVSMIAQSVTAVALGLSYPPDYRRMM 240
QY 240 QSGRKGADIMYTGVDGCRKIADDEGAKAFKGMNSVLRMGGAFLVLYDEIKKY 296
DB 241 QSGRKGADIMYTGVDGCRKIADDEGAKAFKGMNSVLRMGGAFLVLYDEIKKY 297

RESULT 9

S31935
ADP,ATP carrier protein - African malaria mosquito
C;Species: Anopheles gambiae (African malaria mosquito)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S31935; S31936
R;Beard, C.B.; Crews-Oyen, A.E.; Collins, F.H.
submitted to the EMBL data library, February 1993
A;Description: A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae.
A;Reference number: S31935
A;Accession: S31935
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-301 <BEA>
A;Cross-references: EMBL:Z21814; EMBL:Z21815
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: duplication; transmembrane protein
F;7-101/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F;112-204/Domain:	ADP,ATP carrier protein repeat	homology <ACP2>
F;209-300/Domain:	ADP,ATP carrier protein repeat	homology <ACP3>

Query Match	73.6%	Score 1142.5	DB 1	Length 301
Best Local Similarity	76.2%	Pred. No. 8.8e-96		
Matches 221	Conservative 26	Mismatches 42	Indels 1	Gaps 1

```
QY      6 WSLFDFLAGVAANAASKTAVAPIERVKLLQVHASKQISAEEKYKGIIDCVRRIPKEQ 65
         : | ||||| ::||| ||||| : ||||| : |||||
Db       8 YGFADFFLAGGISAAASKTAVAPIERVKLLQVHASKQIAVDKQYKGIVDQCFVRIPKEQ 67
```

Dy 66 GFLSWRGINLVIRYPTQLNFAFDKYYQLFLGGVDRHQFWRRFAGNLASGGAAGA 125

Dd 68 GIGAFCCGNLNVIRYPTQLNFAFDVYQVFLGGVDKNTQFWRYFLGNLSGGGAAGA 127

Oy 126 TSLCVYPLDFAFRLADVGRRA-QREFHGLGDCIIKI PKSDGLRGIYQGPNVSVOGII 184
| | | | | : | | | | |
Db 128 TSLCVYPLDFAFRLGADVPGAGEREFNGLDCLKTIVASDGIIGIIRGFNVSVGGII 187

Oy 185 IYKAYFGVVDIAKGMLPDPKNVIHFSMMAQSVAIVAGLLISYPFTVRRRMMQSRK 244
| | | | | : | | | | | : :: | | | | |
Db 188 IYRAYFGCIDTAKGMLPDPKNTSIFVSMAAQVTTASGLISYPFTVRRRMMQSWPC 247

Dy 245 GAADIMTIGIVDCWKRILAKDEGAFAFKGASNVLRKMGCAFVLVIDEIK 294
::|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 248 KSEVMYKNTLDCWKIKIGQEGSCAFPKGASNVLRIGGALLVLFYDEVK 297

RESULT 10 :
T25850
hypothetical protein T01B1.4 - *Caenorhabditis elegans*

C:\date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C:\accession: T25850
R:\Geisel, C./Stellies, L.

A:Description: The sequence of C. elegans cosmid T01B11
A:Reference number: Z20099
A:Accession: T25850

A: Molecule type: DNA
A: Residues: 1-313 <GET>
A: Cross-references: EMBL:U80931; PTDN:AB38001.1; GSPDB:GN00022; CESP:T01B11.4

C/Genetics:
A/Gene: CESP:T01B1.4
A/Map position: 4

Cysuperfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Matches	203;	Conservative	36;	Mismatches	49;	Indels	3;	Gaps	2;
Qy	8	FLNDPLAGVAAAVSKTAVAPRIERVKLLIQVQHSKQISAKQYKGIIDCVRIIPKQEGF	67						

Db 25 FLIDLASGGTAAAVSKTAIVAPIERVLLQVQDASLTIAADRRYKGIADVLRVPKEQGY 84

Dy 68 LSFWRGNLANVIRYPTOALNPAFKDKYKQFLGGVDRHKQFWRRYFAGNLASGGAAGTS 127

DB 85 AALMRGNLANVIRYFPTQALNFAFKDTYKNIFQKGDKKDQFKRFGNLTASGGACGATS 144

DY 128 LCFVYPLDPAKTRLAADVGRRAQREPHGLDCCIITKFKSDGIRGLYQGFNNVSVOGIIITYR 187

143 LCFVIFPDEFAKIKLMDVGNKNEREFKSLMDCLVKNLSDFGLKNGFVSQGLIIIR 204
QY 188 AAFGVYDTAKGML--PDPKNVHIFVSMIAQSVTVAGLLSYFPDTVRRMMQSGRKA 246

247 DIMYGTVDQWRKIADDEGAKAFPKGAMSNVLRMGGAFTVLVLYDEIKRYV 297

RESULT 11

C1Species: *Caenorhabditis elegans*
 hypotheical protein K01H12.2 - *Caenorhabditis elegans*
 C1Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text change 11-Jan-2000
 C1Accession: T33207

K/McMurray, A.
submitted to the EMBL Data Library, December 1995
A/Reference number: Z19707
A/Accession: T23207

A1.Cross-references: EMBL:Z68318; P1DN:CAA92472.1; GSPDB:GN00022; CESP:X01H12.2
A1.Residues: 1-313 <MIL>
A1.Molecule type: DNA
A1.status: preliminary; translated from GB/EMBL/DDBJ

n/Experimental source: clone 101112
 C:Genetic8:
 A:Gene: CESP:K01H12.2
 A:Map position: 4

Query Match	67.2%	Score 1043.5	DB 2	Length 313
C:Superfamily: ADF,ATP carrier protein; ADF,ATP carrier protein repeat homology				

8	FLKDFLAGVAALVSKTAVAPIERVKLLQVHASKOISABKQYGIIDCVRIPEQGF	67
Matches	202; Conservative 37; Mismatches 49; Indels 3; Gaps 2.	

Db 25 FLIDLASGCTAAAVSKTAVAPIERVKLLQVDASLTIAADKRYKGIVDLVVRVPEQGY 84

Qy 68 LSPFRGNLANVIRYPTQALNPAFKOKYKQLFLGVDNRHKQFWRYPAGNLASGGAAGATS 122

Db 85 AALMRGNLANVIRYPTQALNFAFQDTYKNI FQKGLDKDDFWKFPAGNLSGGAAGTS 144

Gy 128 LCFVYPLDFASTRLLADVGRARQREHGLDCCI IKI FKSDELRLGLVQGFNNVSGIITIR 187

Db 145 LCFYVPLDPARTRLADVGKANEREFFKGLADCLVYKIAKSDPRTGLYRGFFVSVQGIITYYR 204

Qy 188 AAYGVGYDTAKGML-PDPKNVHI FVSWMLAQSVTAVAGLLSYPRDTYRRRMQSGRGA 246

Db 205 AAYGMEPIAKMVFADGKLNFFAAWALNQVLTGSGGISYPMQIVRRRMNQSGKK-- 262

Db 263 DVLKNTLDCAVKLIKKEGMSAMEFGALSNVFRGTGALVLAIDEIQFI 313

hypothetical protein T27B9.1 - *Caenorhabditis elegans*
T25371
Cispecies: *Caenorhabditis elegans*
C.Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #feat change 11-Jan-2000

C:Accession: 1253/1
R: Lloyd, C.
Submitted to the EMBL Data Library, November 1996
A: Reference number: Z20024

A:Accession: 125371
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-300 <WIL>

M10088: references: PMID:2024037; FUND:CB007679.1; GEFDB:G000022; CBSE:127B9.2
 A:Experimental source: clone T27B9
 C:Genetics:
 A:Gene: CBSP:T27B9.1

a:introns: 20/1; 41/3; 115/2
c:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Best Local Similarity 69.1%; Pred No. 2, 8e-86;
Matches 201; Conservative 38; Mismatches 49; Gaps 3; Indels 2;

QY 8 FLKDFLAGAANAASKTAVAPIERVKLLQVGHASQISAEKQYGIIDCVIRIPKEGF 67
 DB 12 FLIDIASGTAATAASKTAVAPIERVKLLQVODASAKALAVDRYKGIIMDLARVPEKQGV 71
 QY 68 LSPFMGNLANVIRYPTQALNFAFDKQYKQFLGVDVBHKKQFWRFPAGNLASGGAAGATS 127
 DB 72 AALFMGNLANVIRYPTQALNFAFDKQYKQFLGVDVBHKKQFWRFPAGNLASGGAAGATS 131
 QY 128 LCFVYPLDPARTRLADVGRRAQREPHGIDCIIKIFKSDGLRGLYOGFNNVSVGIIITYR 187
 DB 132 LCFVYPLDPARTRLADVGRRAQREPHGIDCIIKIFKSDGLRGLYOGFNNVSVGIIITYR 191
 QY 188 AAFYEVVITAKGML-PDRKNVHIIFVSMIAQSVTAVALGLSPPTVTRRRMMQSGRKA 246
 DB 192 AAFYEVVITAKGML-PDRKNVHIIFVSMIAQSVTAVALGLSPPTVTRRRMMQSGRKA 249
 QY 247 DIMYGTVDGWRKLIADGAKAFKFGAMSNVLRGNGAFVLTLYDEIKKYV 297
 DB 250 DILYKNTIDCAKKTIONEGSMFPGALSNVFRGTGALVLTLYDEIKKYV 300

RESULT 13

hypochemical protein W02D3.6 - Caenorhabditis elegans
 CSpecies: Caenorhabditis elegans
 CDate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
 CAccession: T15206
 Rile, T.; Weinstein, L.; Rifkin, L.
 submitted to the EMBL Data Library, May 1997
 A:Description: The sequence of C. elegans cosmid W02D3.
 A:Reference number: Z18308
 A:Accession: T15206
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-300 <LET>
 A:Cross-references: EMBL:AF003141; NID:G2088732; PID:G2088738; PIDN:AA854179.1; GSPDB:GN
 A:Experimental source: strain Bristol N2; Clone W02D3
 C:Genetics:
 A:Gene: CESP:W02D3.6
 A:Map position: 1
 C:Superfamily: ADP, ATP carrier protein repeat homology <ACR>
 F:9-103/Domain: ADP, ATP carrier protein repeat homology <ACR>

Query Match 64.7%; Score 1005.5; DB 2; Length 300;
 Best Local Similarity 66.0%; Pred. No. 2-2e-83;
 Matches 192; Conservative 40; Mismatches 56; Indels 3; Gaps 2;
 QY 8 FLKDFLAGAANAASKTAVAPIERVKLLQVGHASQISAEKQYGIIDCVIRIPKEGF 67
 DB 12 FLIDIASGTAATAASKTAVAPIERVKLLQVSDVSETVADKKYGIIMDLARVPEKQGV 71
 QY 68 LSPFMGNLANVIRYPTQALNFAFDKQYKQFLGVDVBHKKQFWRFPAGNLASGGAAGATS 127
 DB 72 AALFMGNLANVIRYPTQALNFAFDKQYKQFLGVDVBHKKQFWRFPAGNLASGGAAGATS 131
 QY 128 LCFVYPLDPARTRLADVGRRAQREPHGIDCIIKIFKSDGLRGLYOGFNNVSVGIIITYR 187
 DB 132 LCFVYPLDPARTRLADVGRRAQREPHGIDCIIKIFKSDGLRGLYOGFNNVSVGIIITYR 191
 QY 188 AAFYEVVITAKGML-PDRKNVHIIFVSMIAQSVTAVALGLSPPTVTRRRMMQSGRKA 246
 DB 192 AAFYEVVITAKGML-PDRKNVHIIFVSMIAQSVTAVALGLSPPTVTRRRMMQSGRKA 249
 QY 247 DIMYGTVDGWRKLIADGAKAFKFGAMSNVLRGNGAFVLTLYDEIKKYV 297
 DB 250 DILYKNTIDCAKKTIONEGSMFPGALSNVFRGTGALVLTLYDEIKKYV 300

RESULT 14
 A41677
 ADP, ATP carrier protein - Chlorella kessleri
 CSpecies: Chlorella kessleri
 CDate: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999

CAccession: A41677
 R.Hilgath, C.; Sauer, N.; Tanner, W.
 J. Biol. Chem. 266, 24044-24047, 1991
 A>Title: Glucose increases the expression of the ATP/ADP translocator and the glyceralde
 A:Reference number: A41677; MUID:92084708; PMID:1748677
 A:Accession: A41677
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-339 <HLI>
 A:Cross-references: GB:M76669; NID:G516596; PIDN:AAA33027.1; PID:G516597
 C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:38-134/Domain: ADP, ATP carrier protein repeat homology <ACPI>
 F:144-235/Domain: ADP, ATP carrier protein repeat homology <AC2>
 F:241-339/Domain: ADP, ATP carrier protein repeat homology <AC3>

Query Match 62.7%; Score 973.5; DB 2; Length 339;
 Best Local Similarity 65.3%; Pred. No. 2e-80;
 Matches 192; Conservative 30; Mismatches 65; Indels 7; Gaps 4;
 QY 7 SFLKDFLAGAANAASKTAVAPIERVKLLQVGHASQISAEK-QYKGIIDCVIRIPKE 64
 DB 40 AFDKDLAAGTAAGTAASKTAVAPIERVKLLQVSDVSETVADKKYGIIMDLARVPEKQGV 99
 QY 65 LSPFMGNLANVIRYPTQALNFAFDKQYKQFLGVDVBHKKQFWRFPAGNLASGGAAG 124
 DB 100 QGVASFMGNLANVIRYPTQALNFAFDKQYKQFLGVDVBHKKQFWRFPAGNLASGGAAG 158
 QY 125 AATLCFVYPLDPARTRLADVGRRAQREPHGIDCIIKIFKSDGLRGLYOGFNNVSVGII 184
 DB 159 AGSLIYPLDPARTRLADVGRRAQREPHGIDCIIKIFKSDGLRGLYOGFNNVSVGII 218
 QY 185 IYRAAYFGVYDTAKGML-PDRKNVHIIFVSMIAQSVTAVALGLSPPTVTRRRMMQSGR 243
 DB 219 YVRGAYFGVYDTAKGML-PDRKNVHIIFVSMIAQSVTAVALGLSPPTVTRRRMMQSGR 276
 QY 244 KGAIDMTGTVDCWRKLIADGAKAFKFGAMSNVLRGNGAFVLTLYDEIKKYV 297
 DB 277 -GGRQYNTGTVDCWRKLIADGAKAFKFGAMSNVLRGNGAFVLTLYDEIKKYV 329

RESULT 15

ADP, ATP carrier protein - malaria parasite (Plasmodium falciparum)
 N:Alternate names: ADP/ATP transporter
 CSpecies: Plasmodium falciparum
 CDate: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jun-2000
 CAccession: S68993; S51132
 R.Hatlin, I.; Baureguberry, G.
 Eur. J. Biochem. 228, 86-91, 1995
 A>Title: Molecular characterization of the ADP/ATP-transporter cDNA from the human malar
 A:Reference number: S68993; MUID:95188918; PMID:7863016
 A:Accession: S68993
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-301 <HAT>
 A:Cross-references: EMBL:X83551; NID:G623334; PIDN:CAA58541.1; PID:G623335
 C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
 C:Keywords: duplication; transmembrane protein
 F:6-102/Domain: ADP, ATP carrier protein repeat homology <ACPI>
 F:112-203/Domain: ADP, ATP carrier protein repeat homology <AC2>
 F:209-301/Domain: ADP, ATP carrier protein repeat homology <AC3>

Query Match 58.2%; Score 904.5; DB 2; Length 301;
 Best Local Similarity 58.3%; Pred. No. 3.1e-74;
 Matches 172; Conservative 46; Mismatches 70; Indels 5; Gaps 4;
 QY 7 SFLKDFLAGAANAASKTAVAPIERVKLLQVGHASQISAEK-QYKGIIDCVIRIPKE 64
 DB 8 NFADFLMGISAAISKTAVAPIERVKLLQVSDVSETVADKKYGIIMDLARVPEKQGV 67
 QY 65 QGFLSPFMGNLANVIRYPTQALNFAFDKQYKQFLGVDVBHKKQFWRFPAGNLASGGAAG 124

Db 68 QGVLSLWGRNVANVIRYFPTQAFNFAFNDYFKNIF-PRYDONTDFSKFPCVNIISGATAG 126
 QY 125 ATSLCFYVPLDFAFTRLAADVGRRAQREHGLGDCIIFKESDGLRGLYOGFNYSVQGI 184
 Db 127 AISLILVPLDFAFTRLAADVGRRAQREHGLGDCIIFKESDGLRGLYOGFNYSVQGI 186
 QY 185 IYRAAYFGVYDTAKGML-PDPKNVHIFVSMIAOSVTAVAGILSYFPTVRRMMOSGR 243
 Db 187 VYRGSYFGLYDSAKALLFTNDKNTNIVLKVAVASVTIILAGLISYFPTVRRMMOSGR 246
 QY 244 KG-ADIMYTGTVDCWRKIADKDGAKAFPKGAMSVNLRGMGAFVLYVDEIKKXV 297
 Db 247 KGKEEIOYKNTIDCWIKILRNKGFGFKGAMSVNLRGMGAFVLYVDEIKKXV 301

Search completed: December 18, 2003, 12:44:04
 Job time : 15.3012 Secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:16:16 ; Search time 8.31467 Seconds
(without alignments)
1679.794 Million cell updates/sec

Title: US-09-811-131-31
Perfect score: 1553
Sequence: 1 MGDHMSFLKDFLAGAVAA.....LRMGGAFLVLYDEIKKYV 297

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1526.5	98.3	298	1 ADT1_HUMAN	P12235 homo sapien
2	1466.5	94.4	298	1 ADT1_RAT	Q05962 rattus norv
3	1463.5	94.2	298	1 ADT1_MOUSE	P49962 mus musculu
4	1453.5	93.6	297	1 ADT1_BOVIN	P02722 bos taurus
5	1408.5	90.7	298	1 ADT2_MOUSE	P51881 mus musculu
6	1407.5	90.6	298	1 ADT2_RAT	Q05073 rattus norv
7	1398.5	90.1	298	1 ADT2_HUMAN	P05141 homo sapien
8	1385.5	89.2	298	1 ADT3_HUMAN	P12236 homo sapien
9	1380.5	88.9	298	1 ADT3_BOVIN	P33007 bos taurus
10	1241	79.9	299	1 ADT_DROME	Q26365 drosophila
11	1162.5	74.9	301	1 ADT_ANOXA	Q21238 anopheles g
12	973.5	62.7	339	1 ADT_CHLKE	P31692 chlorella k
13	770.5	49.6	308	1 ADT_CHLKE	P27080 chlamydomon
14	756.5	48.7	387	1 ADT1_MAIZE	P04709 zea mays (m
15	752.5	48.5	386	1 ADT_SCHPO	Q09188 schizosacch
16	752.5	48.5	386	1 ADT1_GOSHI	Q22342 gossypium h
17	751.5	48.4	382	1 ADT_ORYSA	P31691 oryza sativ
18	751.5	48.4	387	1 ADT2_MAIZE	P11857 zea mays (m
19	746	48.0	381	1 ADT1_ARATH	P25083 arabidopsis
20	744.5	47.9	386	1 ADT1_SOLTU	P41629 triticum ab
21	742.5	47.8	331	1 ADT1_WHEAT	P27081 solanum tub
22	740	47.6	386	1 ADT2_SOLTU	P18238 saccharomyc
23	736	47.4	307	1 ADT3_YEAST	P18239 saccharomyc
24	734	47.3	318	1 ADT2_YEAST	P02723 neurospora
25	733.5	47.1	313	1 ADT1_NEUCR	P40941 arabidopsis
26	731	47.1	385	1 ADT2_ARATH	P43382 kluyveromyc
27	729	46.9	305	1 ADT_KULUA	P41630 triticum ae
28	728.5	46.9	331	1 ADT2_WHEAT	P04710 saccharomyc
29	718.5	46.3	309	1 ADT1_YEAST	Q07574 homo sapien
30	302.5	19.5	678	1 CMCI_HUMAN	Q01888 bos taurus
31	300.5	19.3	330	1 GPC_BOVIN	Q19529 caenorhabdi
32	296.5	19.1	565	1 CMCI_CABEL	Q21153 caenorhabdi
33	296.5	19.1	702	1 CMCI_CABEL	

34	296	19.1	588	1 CMCI_CABEL	Q20799 caenorhabdi
35	295	19.0	322	1 GPC_RAT	P16261 rattus norv
36	292.5	18.8	307	1 GPC2_YEAST	Q99297 saccharomyc
37	292	18.8	332	1 GPC_HUMAN	P16260 homo sapien
38	291	18.7	675	1 CMCI_HUMAN	Q94180 homo sapien
39	280	18.0	315	1 MFT_HUMAN	Q942d1 homo sapien
40	279.5	18.0	676	1 CMCI_MOUSE	Q96xx4 mus musculu
41	270.5	17.4	315	1 SA18_HUMAN	Q941k4 homo sapien
42	267.5	17.2	325	1 UCP5_MOUSE	Q942b2 mus musculu
43	265.5	17.2	310	1 UCP1_YEAST	Q03028 saccharomyc
44	265.5	17.1	325	1 UCP5_HUMAN	Q95258 homo sapien
45	263.5	17.0	695	1 CMCI_DROME	Q94a73 drosophila

ALIGNMENTS

RESULT 1
ID ADT1_HUMAN STANDARD, PRT, 298 AA.
AC P12235
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
GN SLIC25A4 OR ANT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89236396; PubMed=2541251;
RA Cozens A.L., Runswick M.J., Walker J.E.;
RT "DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP translocase.";
RL J. Mol. Biol. 206:261-280(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89340499; PubMed=2547778;
RA Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J., Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;
RT "A human muscle adenine nucleotide translocator gene has four exons, is located on chromosome 4, and is differentially expressed.";
RL J. Biol. Chem. 264:13998-14004(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88041149; PubMed=2823266;
RA Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;
RT "cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader peptide, divergence from a fibroblast translocator cDNA, and coevolution with mitochondrial DNA genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Straube R.L., Feringold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F., Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loguailano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Holik S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
 RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [5]
 RN SEQUENCE OF 1-37 FROM N.A.
 RN TISSUE=Liver;
 RC MEDLINE=88124845; PubMed=2829183;
 RA Houldsworth J., Attardi G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
 RT level in adult human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381 (1988).
 RN [6]
 RN VARIANTS PEO PRO-114 AND MET-289.
 RX MEDLINE=20385067; PubMed=10926541;
 RA Karkonen J., Junesius J.K., Tirant V., Kyttala A., Zeviani M.,
 RA Comi G.P., Keranen J., Peltonen L., Suomalainen A.;
 RT "Role of adenine nucleotide translocator 1 in mtDNA maintenance.";
 RL Science 289:782-785 (2000).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- DISEASE: Defects in SLC25A4 are a cause of autosomal dominant
 CC progressive external ophthalmoplegia with various mitochondrial
 CC DNA deletions (PEO). Patients with PEO have mitochondrial
 CC myopathy, progressive external ophthalmoplegia, and other
 CC abnormalities associated with multiple different deletions of
 CC mitochondrial DNA.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC
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 CC
 CC EMBL, J02966; AAA61223.1; -;
 CC EMBL, J03593; AAA36751.1; -;
 CC EMBL, J04982; AAA51736.1; -;
 CC EMBL, BC008664; AAH08664.1; -;
 CC PIR, A44778; A44778.
 CC Gene, HGNC:10990; SLC25A4.
 CC MIM, 103220; -;
 CC MIM, 157640; -;
 CC GO, GO:0005887; C:integral to plasma membrane; TAS.
 CC GO, GO:0005739; C:mitochondrion; TAS.
 CC GO, GO:0015207; F:adenine transporter activity; TAS.
 CC GO, GO:0006091; F:energy pathways; TAS.
 CC GO, GO:0000002; F:mitochondrial genome maintenance; TAS.
 CC GO, GO:0006832; F:small molecule transport; TAS.
 CC InterPro, IPR002067; Mlt carrier.
 CC InterPro, IPR002030; Mlt uncoupling.
 CC InterPro, IPR001993; Mitochondrial carrier.
 CC Pfam, PF00153; mito_carr_3.
 CC PRINTS, PR00926; MITOCARRIER.
 CC PRINTS, PR00784; MTNDCOUPLING.
 CC PROSITE, PS00215; MITOCH CARRIER; 3.
 KW Mitochondrion, Inner membrane, Repeat, Transmembrane, Transport;
 KW Multigene family, Disease mutation.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 208 2.

FT REPEAT 209 298 3.
 FT VARIANT 114 114 A->P (IN PEO).
 FT VARIANT 289 289 /FTID=VAR 012111.
 FT VARIANT 289 289 V->M (IN PEO).
 FT VARIANT 289 289 /FTID=VAR 012112.
 FT CONFLICT 16 16 G->A (IN REF. 3).
 FT CONFLICT 147 149 KGA->RR (IN REF. 3).
 FT CONFLICT 227 227 V->L (IN REF. 3).
 SQ SEQUENCE 298 AA; 33064 MW; 59F0DFAC4E7CFFB CRC64;
 Query Match 98.3%; Score 1526.5; DB 1; Length 298;
 Best Local Similarity 98.3%; Pred. No. 2e-129;
 Matches 293; Conservative 2; Mismatches 2; Indels 1; Gaps 1;
 QY 1 MGDHMSFLKDFLAGAVALAAVSKTAVADIEBVKLLQVQHSKQISAEKQYKGIIDCVR 60
 DB 1 MGDHMSFLKDFLAGAVALAAVSKTAVADIEBVKLLQVQHSKQISAEKQYKGIIDCVR 60
 QY 61 IPKEGFLSPWRGNLANVIRFPPOALNPAFKDKYKQLFLGVDNRHQPFRYFAGNLASG 120
 DB 61 IPKEGFLSPWRGNLANVIRFPPOALNPAFKDKYKQLFLGVDNRHQPFRYFAGNLASG 120
 QY 121 GAAGTSLCFYYPIDPARTRLAADVGR-RAQREFHGLDCTIKTIPKSDGLKGLYOGFNVS 179
 DB 121 GAAGTSLCFYYPIDPARTRLAADVGR-RAQREFHGLDCTIKTIPKSDGLKGLYOGFNVS 180
 QY 180 VQGIIVYAAVFGYDTAKGMLPDKNVHIFVSWMIAGSVTAVALGLSYPEDTVRRMM 239
 DB 181 VQGIIVYAAVFGYDTAKGMLPDKNVHIFVSWMIAGSVTAVALGLSYPEDTVRRMM 240
 QY 240 QSGKRGADIMTGVDCRRTAKDEGAKAFKGMNSVLRGMGAFTVYLDEIKKYV 297
 DB 241 QSGKRGADIMTGVDCRRTAKDEGAKAFKGMNSVLRGMGAFTVYLDEIKKYV 298
 RESULT 2
 ADT1 RAT STANDARD, PRT, 298 AA.
 AC Q05962;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
 GN translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
 DE SLC25A4 OR ANT1.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley, and Wistar; TISSUE=Heart, and Liver;
 RX MEDLINE=94002161; PubMed=8399300;
 RA Shinohara Y., Kamada M., Yamazaki N., Terada H.;
 RT "Isolation and characterization of cDNA clones and a genomic clone
 RT encoding rat mitochondrial adenine nucleotide translocator.";
 RL Biochem. Biophys. Acta 1152:192-196 (1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER
 CC EXTENT, IN BRAIN AND KIDNEY.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC
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CC EMBL; X61667; CA43842.1; -
 DR EMBL; D12770; BAA02237.1; -
 DR PIR; I60173; I60173.
 DR InterPro; IPR002067; Mlt carrier.
 DR InterPro; IPR002030; Mlt uncoupling.
 DR InterPro; IPR001993; Mitoch carrier.
 DR Pfam; PF00153; mito_carr; 3_
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH CARRIER; 3.
 DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32389 MW; 66704FF78C6BC320 CRC64;

Query Match 94.4%; Score 1466.5; DB 1; Length 298;
 Best Local Similarity 94.3%; Pred. No. 4.7e-124;
 Matches 281; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDHAWFLKDFLAGAANAASVKTAVPIERVKLLQVQASKOISAEKQYKGIIDCVNR 60
 1 MGDALFLKDFLAGAANAASVKTAVPIERVKLLQVQASKOISAEKQYKGIIDCVNR 60
 DB 1 IPKQGFSLFWRGMLANVIRYFPQALNFAFKDKYKOLFLGCVDRHQPMRYFAGNLSG 120
 61 IPKQGFSLFWRGMLANVIRYFPQALNFAFKDKYKOLFLGCVDRHQPMRYFAGNLSG 120
 DB 1 IPKQGFSLFWRGMLANVIRYFPQALNFAFKDKYKOLFLGCVDRHQPMRYFAGNLSG 120
 61 IPKQGFSLFWRGMLANVIRYFPQALNFAFKDKYKOLFLGCVDRHQPMRYFAGNLSG 120
 QY 121 GAAATSLCFYPPDPATRIAAVGR-RAGREFHGGDCLIKFKSDGLGLYQGFNV 179
 121 GAAATSLCFYPPDPATRIAAVGR-RAGREFHGGDCLIKFKSDGLGLYQGFNV 179
 DB 121 GAAATSLCFYPPDPATRIAAVGR-RAGREFHGGDCLIKFKSDGLGLYQGFNV 179
 121 GAAATSLCFYPPDPATRIAAVGR-RAGREFHGGDCLIKFKSDGLGLYQGFNV 179
 QY 180 VQGIITRAAFYGYDTAKGLPDPKVVHLFVSMIAQSVTAVALGLSYPPDYRRMM 239
 181 VQGIITRAAFYGYDTAKGLPDPKVVHLFVSMIAQSVTAVALGLSYPPDYRRMM 240
 DB 181 VQGIITRAAFYGYDTAKGLPDPKVVHLFVSMIAQSVTAVALGLSYPPDYRRMM 240
 181 VQGIITRAAFYGYDTAKGLPDPKVVHLFVSMIAQSVTAVALGLSYPPDYRRMM 240
 QY 240 QSGRKGADIMTGTVCWRKIADEGAKAFKGMVNLGSGAPVLYLDEIKKYV 297
 241 QSGRKGADIMTGTVCWRKIADEGAKAFKGMVNLGSGAPVLYLDEIKKYV 298
 DB 241 QSGRKGADIMTGTVCWRKIADEGAKAFKGMVNLGSGAPVLYLDEIKKYV 298
 241 QSGRKGADIMTGTVCWRKIADEGAKAFKGMVNLGSGAPVLYLDEIKKYV 298

RESULT 3
 ADIT_MOUSE STANDARD; PRT; 298 AA.
 ID ADIT_MOUSE
 AC P48962; O62164;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
 translocase 1) (Adenine nucleotide translocator 1) (ANT 1) (MANC1).
 GN SLC25A4 OR ANT1 OR ANCI.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RX STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=97059403; PubMed=8903724;
 RA Ellisen J.W., Li X., Francke U., Shapiro L.J.;
 RT "Rapid evolution of human pseudautosomal genes and their mouse
 homologs.";
 RL Mamm. Genome 7:25-30(1996).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Muscle;
 RA Laplace C., Cochet P.;
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Levy S.B., Chen Y.-S., Graham B.H., Wallace D.C.;
 RT "Expression and sequence analysis of the mouse adenine nucleotide
 translocase 1 and 2 genes.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bye;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strauberg R.L., Pelngold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gnatratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren R.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield A.S.N., Krzywanski M.I., Skalka U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -I- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 MITOCHONDRIAL INNER MEMBRANE.
 CC -I- SUBUNIT: Homodimer.
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 inner membrane.
 CC -I- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -I- SIMILARITY: Belongs to the mitochondrial carrier family.
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CC EMBL; U27315; AAC52837.1; -
 DR EMBL; X74510; CA52616.1; -
 DR EMBL; AP240002; AAP64470.1; -
 DR EMBL; BC003791; AAH03791.1; -
 DR EMBL; BC026925; AAH26925.1; -
 DR PIR; S37210; S37210.
 DR MGD; MGI:1353495; SLC25A4.
 DR InterPro; IPR002067; Mlt carrier.
 DR InterPro; IPR002030; Mlt uncoupling.
 DR InterPro; IPR001993; Mitoch carrier.
 DR Pfam; PF00153; mito_carr; 3_
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH CARRIER; 3.
 DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.

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FT REPEAT      111 208 2.
FT REPEAT      209 298 3.
FT CONFLICT    136 136 F -> L (IN REF. 1).
SQ SEQUENCE    298 AA; 32904 MW; 3A849FEAB0981462 CRC64;

Query Match
Beef Local Similarity 94.2%; Score 1463.5; DB 1; Length 298;
Matches 280; Conservative 10; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGVAANAASKTAVAPIERKLLQVOHASKQISAEKQYKGIIDCVVR 60
DB 1 MGDQSLSTLKDFLAGGIAAASKTAVAPIERKLLQVOHASKQISAEKQYKGIIDCVVR 60
QY 61 IPKEGGLSPFMRGNLANVIRYPTQALNPAFKDKTKQLFLGVDVRHKQFWRYPAGNLASG 120
DB 61 IPKEGGLSPFMRGNLANVIRYPTQALNPAFKDKTKQLFLGVDVRHKQFWRYPAGNLASG 120
QY 121 GAAGATSTCFVYPLDPARTRLAADVGR-RAQREPHGLDGCIIKIKPSDGLRGLYOGFVVS 179
DB 121 GAAGATSTCFVYPLDPARTRLAADVGR-RAQREPHGLDGCIIKIKPSDGLRGLYOGFVVS 179
QY 180 VQGIITVYAAVFGVYDTAKGMLPDPKNVHIFVSMNIAOSVTAVALISYEPDVRBRMM 239
DB 180 VQGIITVYAAVFGVYDTAKGMLPDPKNVHIFVSMNIAOSVTAVALISYEPDVRBRMM 239
QY 240 QSGRKGADIMYTGTVDCWRKIAKDEGANAFFKGAWSNVLKMGAFVLVYDEIKKYV 297
DB 240 QSGRKGADIMYTGTVDCWRKIAKDEGANAFFKGAWSNVLKMGAFVLVYDEIKKYV 297
DB 241 QSGRKGADIMYTGTVDCWRKIAKDEGANAFFKGAWSNVLKMGAFVLVYDEIKKYV 298

RESULT 4
ADT1_BOVIN
ID ADT1_BOVIN STANDARD; PRT; 297 AA.
AC P02722;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DB ADP_ATP carrier protein, heart isoform 1 (ADP/ATP translocase 1)
DE (Adenine nucleotide translocator 1) (ANT 1).
GN SLT25A4 OR ANT1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89229693; PubMed=2540808;
RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
RL differences in various tissues.";
RL Biochemistry 28:866-873 (1989).
RN [2]
RP SEQUENCE.
RX MEDLINE=82188267; PubMed=7076130;
RA Aquila H., Miera D., Eulitz M., Klingenberg M.;
RT "Complete amino acid sequence of the ADP/ATP carrier from beef heart
RL mitochondria.";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:345-349 (1982).
RN [3]
RP SEQUENCE OF 207-297 FROM N.A.
RX MEDLINE=86295775; PubMed=3017341;
RA Raemussen U.B., Wohlrad H.;
RT "Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and
RL an unusually short 3'-noncoding sequence.";
RL Biochem. Biophys. Res. Commun. 138:850-857 (1986).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

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CC
DR EMBL; M13783; AAA0363.1; -
DR EMBL; M24102; AAA0768.1; -
DR PIR; A43646; XMB0.
DR InterPro; IPR002067; Mit_carrier.
DR InterPro; IPR002030; Mit_uncoupling.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUOCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KM Multigene family; Methylation.
FT INIT MET 0 0
FT MOD RES 1 1 BLOCKED.
FT TRANSMEM 11 51 METHYLATION (POTENTIAL).
FT TRANSMEM 72 28 2 (POTENTIAL).
FT TRANSMEM 116 133 3 (POTENTIAL).
FT TRANSMEM 175 194 4 (POTENTIAL).
FT TRANSMEM 213 230 5 (POTENTIAL).
FT TRANSMEM 272 290 6 (POTENTIAL).
FT REPEAT 1 1 1.
FT REPEAT 111 110 2.
FT REPEAT 208 297 3.
SQ SEQUENCE 297 AA; 32836 MW; A582D3C4A40AEB48 CRC64;

Query Match
Beef Local Similarity 93.6%; Score 1453.5; DB 1; Length 297;
Matches 280; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

QY 3 DHANSFLDKDFLAGVAANAASKTAVAPIERKLLQVOHASKQISAEKQYKGIIDCVVR 62
DB 2 DQALSLFLDKDFLAGVAANAASKTAVAPIERKLLQVOHASKQISAEKQYKGIIDCVVR 61
QY 63 KEQGLSPFMRGNLANVIRYPTQALNPAFKDKTKQLFLGVDVRHKQFWRYPAGNLASGA 122
DB 62 KEQGLSPFMRGNLANVIRYPTQALNPAFKDKTKQLFLGVDVRHKQFWRYPAGNLASGA 121
QY 123 AGATSLCFVYPLDPARTRLAADVGR-RAQREPHGLDGCIIKIKPSDGLRGLYOGFVVS 181
DB 122 AGATSLCFVYPLDPARTRLAADVGR-RAQREPHGLDGCIIKIKPSDGLRGLYOGFVVS 181
QY 182 GIIITVYAAVFGVYDTAKGMLPDPKNVHIFVSMNIAOSVTAVALISYEPDVRBRMM 241
DB 182 GIIITVYAAVFGVYDTAKGMLPDPKNVHIFVSMNIAOSVTAVALISYEPDVRBRMM 241
QY 242 GRKGDIMYTGTVDCWRKIAKDEGANAFFKGAWSNVLKMGAFVLVYDEIKKYV 297
DB 242 GRKGDIMYTGTVDCWRKIAKDEGANAFFKGAWSNVLKMGAFVLVYDEIKKYV 297

RESULT 5
ADT2_MOUSE
ID ADT2_MOUSE STANDARD; PRT; 298 AA.
AC P51881; O61311;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DB ADP_ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLT25A5 OR ANT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=97059403; PubMed=8903724;
 RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
 RT "Rapid evolution of human pseudautosomal genes and their mouse
 homologs";
 RL Mamm. Genome 7:25-30(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RA Sheldon J.G.;
 RL Theis (1995), University of Cambridge, U.K.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv;
 RA Cochet P., Laplace C.;
 RL Submitted (FEB-1993) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP REVISIONS.
 RA Laplace C.;
 RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20432087; PubMed=10974536;
 RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
 RT "Expression and sequence analysis of the mouse adenine nucleotide
 translocase 1 and 2 genes";
 RL Gene 254:57-66(2000).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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 CC -----
 DR EMBL; U27316; AAC52838.1; -;
 DR EMBL; U10404; AA19009.1; -;
 DR EMBL; X70847; CA50196.1; -;
 DR EMBL; AF240003; AAF64471.1; -;
 DR MCD; MGI:1353496; Slc25a5.
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carri; 3-
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32931 MW; 0798E04B987EFE20 CRC64;
 Query Match 90.7%; Score 1408.5; DB 1; Length 298;
 Best Local Similarity 89.6%; Pred. No. 7.3e-119;

Matches 266; Conservative 17; Mismatches 13; Indels 1; Gaps 1;
 QY 1 MGDHMSLKDPLAGAVAAVSKTAVPIREVKILLQVQASKQISAEKQKGIIDCVR 60
 DB 1 MTDAVSPADPLAGVAAAIKSTAVAPIREVKILLQVQASKQITADKQYKGIIDCVR 60
 QY 1PKQGFSPFRGNLVANIRPEPQALNFAPKDXYKQLFLGGVDRHQPFMYPPGNLASG 120
 DB 1PKQGVLSFWRGNLVANIRPEPQALNFAPKDXYKQLFLGGVDRHQPFMYPPGNLASG 120
 QY 121 GAAGATSLCFYVPLDPATRLAADVGR-AGREPHGLDCCIIFKSPDGLNGLYQGFNV 179
 DB 121 GAAGATSLCFYVPLDPATRLAADVGRAGREPHGLDCCIIFKSPDGLNGLYQGFNV 180
 QY 180 VQGIITRAAYFGYDPAKGLPDPKXVHIVSWMIQSVTAVAGLISPPDYRRRRMM 239
 DB 181 VQGIITRAAYFGYDPAKGLPDPKXVHIVSWMIQSVTAVAGLISPPDYRRRRMM 240
 QY 240 QSGRRGADIMVTVDCMRKIAKDEGAKAPFGKAMSVTLRGMGAPVLYVDEIKKY 296
 DB 241 QSGRRGADIMVTVDCMRKIAKDEGAKAPFGKAMSVTLRGMGAPVLYVDEIKKY 297
 RESULT 6
 ADT2 RAT STANDARD; PRT; 298 AA.
 AC Q09073.
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
 DE Adenine nucleotide translocator 2 (ANT 2).
 GN SLc25A5 OR ANT2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=94002161; PubMed=8399300;
 RA Shinozawa Y., Kamida M., Yamazaki N., Terada H.;
 RT "Isolation and characterization of cDNA clones and a genomic clone
 encoding rat mitochondrial adenine nucleotide translocator";
 RL Biochem. Biophys. Acta 1152:192-196(1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 inner membrane.
 CC -1- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND
 SKELETAL MUSCLE.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; D12771; BA02238.1; -;
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carri; 3-
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.

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FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 111 2.
FT REPEAT 209 208 3.
SQ SEQUENCE 298 AA; 32901 MW; 6A59204B987EE35 CRC64;

Query Match
Beet Local Similarity 89.6%; Score 1407.5; DB 1; Length 298;
Matches 266; Conservative 16; Mismatches 14; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAAGVAASKTAVAPIERVKLLQVQHASKOISAEKQYGIIDCVR 60
DB 1 MTDAAVSFAKDFLAGVAASIKTAAPIERVKLLQVQHASKOITADKQYGIIDCVR 60
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDHRKQFWRYPAGNLASG 120
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDKRTQFWRYPAGNLASG 120
QY 121 GAAGTSLCFVYPLDPAFRRILADYGR-ACREPHGLDGCIIKIKRSGRLTQYGFVNS 179
DB 121 GAAGTSLCFVYPLDPAFRRILADYGR-ACREPHGLDGCIIKIKRSGRLTQYGFVNS 180
QY 180 VQGIITPAAVYRGVYDTAKGMLPDPKXNHIFSWMIAOSVTAAGLSTYPTVRRMM 239
DB 181 VQGIITPAAVYRGVYDTAKGMLPDPKXNHIFSWMIAOSVTAAGLSTYPTVRRMM 240
QY 240 QSGRRGADIMYTGIVDCWRKIAXDEGAKAFKFGANSVLRGNGAFVLVYDEIKKY 296
DB 241 QSGRRGADIMYTGIVDCWRKIAXDEGAKAFKFGANSVLRGNGAFVLVYDEIKKY 297

RESULT 7
ADT2_HUMAN STANDARD; PRT; 298 AA.
ID AC P05141; O43350;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=90375457; PubMed=2168878;
RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Wuzel J.;
RT "The human fibroblast adenine nucleotide translocator gene. Molecular
RT cloning and sequence."
RL J. Biol. Chem. 265:16060-16063(1990).
RN RP SEQUENCE FROM N.A.
RX MEDLINE=87166056; PubMed=3031073;
RA Battini R., Ferrari S., Kaczmarek L., Calabretta B., Chen S.T.,
RA Baserga R.;
RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
RT growth-regulated."
RL J. Biol. Chem. 262:4355-4358(1987).
RN RP SEQUENCE FROM N.A.
RA Chen C.N., Su Y., Baybayan P., Simino A., Nagaraia R.,
RA Mazarek R.A., Schlesinger D., Chen R.Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN RP SEQUENCE FROM N.A.

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RA Becker M., Graves T., Ozereky P.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 47-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houldsworth J., Altardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver."
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; M57424; AAA51737.1; -
CC EMBL; J02683; AAA35579.1; -
CC EMBL; L78810; AAB39266.1; -
CC EMBL; AC004000; AAB96347.1; -
CC EMBL; J03591; AAA36749.1; -
CC PIR; A29132; A29132.
CC Genew; HGNC:10991; SLCA5A5.
CC MIM; 300150; -
CC GO; GO:0005887; C:Integral to plasma membrane; TAS.
CC GO; GO:0015207; P:adenine transporter activity; TAS.
CC GO; GO:0006832; P:small molecule transport; TAS.
CC InterPro; IPR002067; Mlt_carrier.
CC InterPro; IPR002030; Mlt_uncoupling.
CC InterPro; IPR001993; Mitoch_carrier.
CC Pfam; PF00153; mltoc_carr; 3-
CC PRINTS; PR00926; MITOCARRIER.
CC PRINTS; PR00784; MTNCOUPLING.
CC PROSITE; PS00215; MITOCH_CARRIER; 3.
CC KX Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
CC KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 111 2.
FT REPEAT 209 208 3.
FT REPEAT 209 298 3.
FT CONFLICT 6 6 V->L (IN REF. 2).
FT CONFLICT 66 66 G->E (IN REF. 2).
FT CONFLICT 111 111 R->L (IN REF. 4 AND 5).
FT CONFLICT 162 162 V->G (IN REF. 5).
SQ SEQUENCE 298 AA; 32895 MW; F973C3AED92C49D3 CRC64;

Query Match
Beet Local Similarity 89.9%; Score 1398.5; DB 1; Length 298;
Matches 264; Conservative 17; Mismatches 15; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAAGVAASKTAVAPIERVKLLQVQHASKOISAEKQYGIIDCVR 60
DB 1 MTDAAVSFAKDFLAGVAASIKTAAPIERVKLLQVQHASKOITADKQYGIIDCVR 60
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDHRKQFWRYPAGNLASG 120
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDKRTQFWRYPAGNLASG 120

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QY 121 GAAGATSLCFYVPLDPFARTLADVGRR-AQREPHGLGDCITIKIFKSDGLNGLYOGFNV 179
 DB 121 GAAGATSLCFYVPLDPFARTLADVGRR-AQREPHGLGDCITIKIFKSDGLNGLYOGFNV 180
 QY 180 VGGIITIRAAVFGYVDTAKGMLPDPKRVHIFVSMVIAQSVTAVALGLSYPPDYRRRMM 239
 DB 181 VGGIITIRAAVFGYVDTAKGMLPDPKRVHIFVSMVIAQSVTAVALGLSYPPDYRRRMM 240
 QY 240 QSGRKGADIMYTGVDGCRKTIADGKAFKAGFPGKMSNVLKMGGAFTLVLYDELKTY 296
 DB 241 QSGRKGADIMYTGVDGCRKTIADGKAFKAGFPGKMSNVLKMGGAFTLVLYDELKTY 297
 RESULT 8
 ADT3_HUMAN STANDARD; PRT; 298 AA.
 ID ADT3_HUMAN STANDARD; PRT; 298 AA.
 AC P1236; Q96C49;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE ADP, ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3)
 DE (Adenine nucleotide translocator 3) (ANT 3).
 GN SLIC25A6 OR ANT3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89236396; PubMed=2541251;
 RA Cozens A.L., Runswick M.J., Walker J.E.;
 RT "DNA sequences of two expressed nuclear genes for human mitochondrial
 ADP/ATP translocase";
 RL J. Mol. Biol. 206:261-280 (1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,
 RA Margolin J.F.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, Cervix, Eye, and Lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Halys S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmitt J., Myers R.M.,
 RA Butlerfield J.S.N., Krzywinski M.I., Skalska U., Smallus D.B.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [4]
 RP SEQUENCE OF 36-298 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=88124845; PubMed=2829183;
 RA Houldsworth J., Altardi G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
 level in adult human liver";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381 (1988).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.

CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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 CC -----
 CC EMBL: J03592; AAA6750.1; -;
 CC EMBL: AY007135; AAG01998.1; -;
 CC EMBL: BC007295; AAH07295.1; -;
 CC EMBL: BC007850; AAH07850.1; -;
 CC EMBL: BC008737; AAH08737.1; -;
 CC EMBL: BC008935; AAH08935.1; -;
 CC EMBL: BC014775; AAH14775.1; -;
 CC PIR: S03894; S03894.
 CC GeneW: HGNC:10992; SLIC25A6.
 CC MIM: 300151; -;
 CC GO: GO:0005744; C:mitochondrial inner membrane translocase co. . .; TAS.
 CC GO: GO:0005471; F:ATP/ADP antiporter activity; TAS.
 CC GO: GO:0006854; P:ATP/ADP exchange; TAS.
 CC InterPro: IPR002067; Mlt_carrier.
 CC InterPro: IPR002030; Mlt_uncoupling.
 CC InterPro: IPR001993; Mitoch_carrier.
 CC Pfam: PF00153; mltc_carri; 3_
 CC PRINTS: PR00926; MITOCARRIER.
 CC PROSITE: PRO0784; MTNCOUPLING.
 CC PROSITE: PS00215; MITOCH_CARRIER; 3.
 CC KX Mitochondrial inner membrane; Repeat; Transmembrane; Transport;
 CC KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 100 1.
 FT REPEAT 101 208 2.
 FT REPEAT 209 298 3.
 FT REPEAT 105 108 3.
 FT CONFLICT 242 242 KHTQ -> RHA (IN REF. 4).
 FT CONFLICT 242 242 S -> F (IN REF. 3; AAH14775).
 SQ SEQUENCE 298 AA; 32866 MW; 18534E9F0E49672F CRC64;
 Query Match 89.2%; Score 1385.5; DB 1; Length 298;
 Best local similarity 87.2%; Pred. No. 8.4e-117;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
 QY 1 MGDHANSFLDPLAGAAVAAVSKTAVAPIRVYKLLGVQVHAKOISAEKQYKGIIDCVVR 60
 DB 1 MTEQALSPADDFLAGGIAAISKTAVAPIRVYKLLGVQVHAKOISAEKQYKGIIDCVVR 60
 QY 61 IPKQGLSFWRGNLANVIRFPTQALNPAFKDKYKQLPLGVDVRHQFMRYPFAGNLASG 120
 DB 61 IPKQGLSFWRGNLANVIRFPTQALNPAFKDKYKQLPLGVDVRHQFMRYPFAGNLASG 120
 QY 121 GAAGATSLCFYVPLDPFARTLADVGRR-AQREPHGLGDCITIKIFKSDGLNGLYOGFNV 179
 DB 121 GAAGATSLCFYVPLDPFARTLADVGRR-AQREPHGLGDCITIKIFKSDGLNGLYOGFNV 180
 QY 180 VGGIITIRAAVFGYVDTAKGMLPDPKRVHIFVSMVIAQSVTAVALGLSYPPDYRRRMM 239
 DB 181 VGGIITIRAAVFGYVDTAKGMLPDPKRVHIFVSMVIAQSVTAVALGLSYPPDYRRRMM 240
 QY 240 QSGRKGADIMYTGVDGCRKTIADGKAFKAGFPGKMSNVLKMGGAFTLVLYDELKTY 297
 DB 241 QSGRKGADIMYTGVDGCRKTIADGKAFKAGFPGKMSNVLKMGGAFTLVLYDELKTY 298

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Rulp D., Lai Z.,
 RA Lesko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mekulov G., Milshina N.V., Nobary C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusseren D.R., Pacle J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Styrekas R., Tector C., Turner R., Venter B., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Zibbe A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Berkeley; TISSUE-larva, Ovary, and Pupae;
 RX MEDLINE=22426066; PubMed=12537569;
 RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champagne M.,
 RA George R.A., Guarin H., Krommiller B., Pacle J.M., Park S., Wan K.H.,
 RA Rubin G.M., Celniker S.E.;
 RT "A *Drosophila* full-length cDNA resource.";
 RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
 CC -1- FUNCTION: Catalyzes the exchange of ADP and ATP across the
 CC mitochondrial inner membrane.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane (By similarity).
 CC -1- DOMAIN: Composed of three homologous domains.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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Query Match 79.9%; Score 1241; DB 1; Length 299;
 Best Local Similarity 79.7%; Pred. No. 7, 3e-104;
 Matches 232; Conservative 26; Mismatches 33; Indels 0; Gaps 0;
 QY 5 AMSFLADPLAGAAVAASKTAVAPIERVKLLQYHASKOISAKQYKGIIDCVRIKPE 64
 DB 7 AVGVKDFPAAGISAAVSKTAVAPIERVKLLQYHASKOISAKQYKGIIDCVRIKPE 66
 QY 65 QGFLSFVRGMLANVIRFPFQALNFAKDKYKQLFLGVDNRHQFMFYPFAGNLASGGAAG 124
 DB 67 QGFSFVRGMLANVIRFPFQALNFAKDKYKQLFLGVDNRHQFMFYPFAGNLASGGAAG 126
 QY 125 ATSLCFYPLDFARTRLAADVGRRAOREFGLGDCIIXIPKSDGLRGLYOGFNVSGI 184
 DB 127 ATSLCFYPLDFARTRLAADVGRRAOREFGLGDCIIXIPKSDGLRGLYOGFNVSGI 186
 QY 185 IYRAAYFGVYDTAKGMLPDKRNHIFVSMIAQSVTAAGLISYFPDVRBRMMQSGRK 244
 DB 187 IYRAAYFGVYDTAKGMLPDKRNHIFVSMIAQSVTAAGLISYFPDVRBRMMQSGRK 246
 QY 245 GADIMYGTGDCWRKIAKDGAKAFKGAASNTLRGGAFLVLYNREIK 295
 DB 247 ATEVYNTLHCWATLAKQEGTGAFFKGAASNTLRGGAFLVLYNREIK 297
 RESULT 11
 ADT_ANOGA STANDARD; PRT; 301 AA.
 ID ADT_ANOGA
 AC Q27238;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
 DE translocator) (ANT).
 OS Anopheles gambiae (African malaria mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Anopheles.
 OX NCBI_TaxID=7165;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=G3;
 RX MEDLINE=94348635; PubMed=8069414;
 RA Beard C.B., Crews-Owen A.B., Kumar V.K., Collins F.H.;
 RT "A cDNA encoding an ADP/ATP carrier from the mosquito *Anopheles*
 RT gambiae.";
 RL Insect Mol. Biol. 3:35-40(1994).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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FT TRANSMEM 178 197 4 (POTENTIAL).
 FT TRANSMEM 216 233 5 (POTENTIAL).
 FT TRANSMEM 275 293 6 (POTENTIAL).
 SQ SEQUENCE 301 AA; 32863 MW; 4CC9E17C9F8DA08B CRC64;
 Query Match 74.9%; Score 1162.5; DB 1; Length 301;
 Best Local Similarity 76.9%; Pred. No. 7.9e-97;
 Matches 223; Conservative 26; Mismatches 40; Indels 1; Gaps 1;
 QY 6 WSFLKPLAGAAVAASVSTAVAPIRVVKLLLOVQASAKQISAEKQYKIIDCVARIPREQ 65
 Db 8 YGFAPKDFLAGGISAASVSTAVAPIRVVKLLLOVQASAKQIANDKQYKIIDCVARIPREQ 67
 QY 66 GFLSFRGNLANVIRYPTQALNPAFAKDKYKQLFLGGVDHKKQFRRYFAGNLASGGAAGA 125
 Db 68 GIGAFWRGNLANVIRYPTQALNPAFAKDKYKQLFLGGVDHKKQFRRYFAGNLASGGAAGA 127
 QY 126 TSLCFVYPLDPAFTRFLADYGRRA-QREFHGIDCIIKIFKSDGLRGLYOGFNVSVOGII 184
 Db 128 TSLCFVYPLDPAFTRFLADYGRRA-QREFHGIDCIIKIFKSDGLRGLYOGFNVSVOGII 187
 QY 185 IYRAAYFGVYDTAKGMLPDPKXVNIIVSWMIASVTAAGLISYPTVRRMMQSGRK 244
 Db 188 IYRAAYFGVYDTAKGMLPDPKXVNIIVSWMIASVTAAGLISYPTVRRMMQSGRK 247
 QY 245 GADIMYGTVDQWCKRIADQEGAKAFPKGAMSNVLRGAGAFVLYLDEIKY 294
 Db 248 KSEVWYKNTLDQWCKRIADQEGAKAFPKGAMSNVLRGAGAFVLYLDEIKY 297
 RESULT 12
 ADT_CHLRE STANDARD; PRT; 339 AA.
 AC P31692;
 DT 01-JUN-1993 (Rel. 26, Last sequence update)
 DT 01-JUN-1993 (Rel. 26, Last sequence update)
 DT 15-OCT-1998 (Rel. 36, Last annotation update)
 DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
 translocator) (ANT).
 OS Chlorella kesselii.
 CC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
 CC Chlorellaceae; Chlorella.
 CC NCBI_TaxID=3074;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92084708; PubMed=1748677;
 RA Hilgarch C., Sauer N., Tanner W.;
 RT "Glucose increases the expression of the ATP/ADP translocator and the
 glyceroldehyde-3-phosphate dehydrogenase genes in Chlorella.";
 RL J. Biol. Chem. 266:24044-24047(1991).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; M76669; AAA33027.1; -.
 DR PIR; A41677; A41677.
 DR InterPro; IPR002067; Mlt carrier.
 DR InterPro; IPR001993; Mitoch carrier.
 DR Pfam; PF00153; mito_carr; 3-
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.

KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 45 62 1 (POTENTIAL).
 FT TRANSMEM 108 126 2 (POTENTIAL).
 FT TRANSMEM 151 168 3 (POTENTIAL).
 FT TRANSMEM 209 228 4 (POTENTIAL).
 FT TRANSMEM 248 265 5 (POTENTIAL).
 FT TRANSMEM 304 322 6 (POTENTIAL).
 SQ SEQUENCE 339 AA; 36686 MW; 54479734A33B3942 CRC64;
 Query Match 62.7%; Score 973.5; DB 1; Length 339;
 Best Local Similarity 65.3%; Pred. No. 7.6e-80;
 Matches 192; Conservative 30; Mismatches 65; Indels 7; Gaps 4;
 QY 7 SFLKPLAGAAVAASVSTAVAPIRVVKLLLOVQASAKQISAEK-QYKIIDCVARIPKE 64
 Db 40 AFVLDLLAGGTAAGISAASVSTAVAPIRVVKLLLOVQASAKQIANDKQYKIIDCVARIPKE 99
 QY 65 GFLSFRGNLANVIRYPTQALNPAFAKDKYKQLFLGGVDHKKQFRRYFAGNLASGGAAGA 124
 Db 100 GGVASFWKGNLANVIRYPTQALNPAFAKDKYKQLFLGGVDHKKQFRRYFAGNLASGGAAGA 158
 QY 125 ATSLCFVYPLDPAFTRFLADYGRRA-QREFHGIDCIIKIFKSDGLRGLYOGFNVSVOGII 184
 Db 159 AGSLIIVYPLDPAFTRFLADYGRRA-QREFHGIDCIIKIFKSDGLRGLYOGFNVSVOGII 218
 QY 185 IYRAAYFGVYDTAKGMLPDPKXVNIIVSWMIASVTAAGLISYPTVRRMMQSGRK 243
 Db 219 IYRAAYFGVYDTAKGMLPDPKXVNIIVSWMIASVTAAGLISYPTVRRMMQSGRK 276
 QY 244 KGDIMYGTVDQWCKRIADQEGAKAFPKGAMSNVLRGAGAFVLYLDEIKY 297
 Db 277 GGERQYNGTVDQWCKRIADQEGAKAFPKGAMSNVLRGAGAFVLYLDEIKY 329
 RESULT 13
 ADT_CHLRE STANDARD; PRT; 308 AA.
 AC P27080;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
 translocator) (ANT).
 OS Arabidopsis thaliana.
 CC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 CC Chlamydomonadaceae; Chlamydomonas.
 CC NCBI_TaxID=3055;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=FUD44-R2;
 RA Sharpe J.A., Day A.;
 RT "Structure, evolution and expression of the mitochondrial ADP/ATP
 translocator gene from Chlamydomonas reinhardtii.";
 RL Mol. Gen. Genet. 237:134-144(1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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 CC
 DR EMBL; X65194; CAA46311.1; -.

DR PIR, S30259; S30259.
 DR InterPro; IPR002067; Mit carrier.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 2.
 DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 74 92 2 (POTENTIAL).
 FT TRANSMEM 116 133 3 (POTENTIAL).
 FT TRANSMEM 178 197 4 (POTENTIAL).
 FT TRANSMEM 217 234 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 SQ SEQUENCE 308 AA; 33528 MM; D47CF0E72B7A53F CRC64;
 Query Match 49.6%; Score 770.5; DB 1; Length 308;
 Best Local Similarity 52.6%; Pred. No. 1e-61;
 Matches 159; Conservative 49; Mismatches 77; Indels 17; Gaps 6;
 QY 7 SFLDPLAGAAVAASVKTAVAPIERVYKLLQVQ-HASQISAQYKGIIDCVIRPEQ 65
 DB 7 NFMVDFLAGGSAASVKTAAPIERVKLLIQNDQMIRGLASPYKIGECFVRYRER 66
 QY 66 GFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFGVDRHKQWRYPAGNLASGAAGA 125
 DB 67 GFLSLMGNLANVIRYPTQALNFAFKDKYKQLFGVDRHKQWRYPAGNLASGAAGA 124
 QY 126 TSLCFVPLDFAFRLADVGR---AOREFHGIDCTIKFKSDGRLGYQFNVSQ 181
 DB 125 VLSLFVYSLDYARFRLANDAKSAGKGGDQFNGLVYRRTIASDGIAGLYRGFNISCV 184
 QY 182 GIITRAYRGVYDTAG-MLPDPKNVHIFVSMIAQSVTAAGLSTPEPTVRRMMQ 240
 DB 185 GIIVYRGLYFGMYSLKPVVLVGPANNFLAFLGWMGITTGAGLASPYDITIRRRMMT 244
 QY 241 SGRKGADIMYGTVDWCRKIAKDEGAKAFKFGANSNVLRGGAFLVLYDEI-----K 294
 DB 245 S---GSANVYSFRHCPQEIYKNEGMSLFRGAGANILRAVAGVLAGYDQLQVILLGK 301
 QY 295 KY 296
 DB 302 KY 303
 RESULT 14
 ADT1 MAIZE STANDARD; PRT; 387 AA.
 ID ADT1 MAIZE STANDARD; PRT; 387 AA.
 DC P04709;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP carrier protein 1, mitochondrial precursor (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
 GN ANTI OR ANT-GI.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.
 OC NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MOTIND-FR7205034;
 RA MEDLINE=9132253; PubMed=1863785;
 RA Winking B.M., Day C.D., Sarah C.J., Leaver C.J.;
 RT "Nucleotide sequence of two cDNAs encoding the adenine nucleotide translocator from Zea mays L.";
 RL Plant Mol. Biol. 17:305-307(1991).
 RN [2]
 RP SEQUENCE OF 59-387 FROM N.A.
 RC STRAIN=CV, B37N;
 RA MEDLINE=89338399; PubMed=2547608;
 RA Leaver C.J., Batchgate B., Baker A.;
 RT "Two genes encode the adenine nucleotide translocator of maize

RT mitochondria. Isolation, characterisation and expression of the structural genes.";
 RL Eur. J. Biochem. 183:303-310(1989).
 RN [3]
 RP SEQUENCE OF 70-387 FROM N.A.
 RX MEDLINE=85297781; PubMed=2994015;
 RA Baker A., Leaver C.J.;
 RT "Isolation and sequence analysis of a cDNA encoding the ATP/ADP translocator of Zea mays L.";
 RL Nucleic Acids Res. 13:5857-5867(1985).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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 CC
 CC EMBL; X57556; CA40781.1; -
 DR EMBL; X15711; CA33742.1; -
 DR EMBL; X02842; CA26600.1; -
 DR PIR; S14876; S14876.
 DR MaizeDB; 17145; -
 DR InterPro; IPR002067; Mit carrier.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 2.
 DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Transic peptide; Multigene family.
 FT TRANSLIT 77 MITOCHONDRION.
 FT CHAIN 78 387 ADP,ATP CARRIER PROTEIN 1.
 FT TRANSMEM 91 108 1 (POTENTIAL).
 FT TRANSMEM 153 171 2 (POTENTIAL).
 FT TRANSMEM 196 213 3 (POTENTIAL).
 FT TRANSMEM 257 276 4 (POTENTIAL).
 FT TRANSMEM 296 313 5 (POTENTIAL).
 FT TRANSMEM 352 370 6 (POTENTIAL).
 FT CONFLICT 102 102 K -> E (IN REF. 2).
 FT CONFLICT 154 154 N -> Y (IN REF. 3).
 SQ SEQUENCE 387 AA; 42391 MM; DE73BB0F478BD57D CRC64;
 Query Match 48.7%; Score 756.5; DB 1; Length 387;
 Best Local Similarity 53.8%; Pred. No. 2.4e-60;
 Matches 164; Conservative 41; Mismatches 77; Indels 23; Gaps 7;
 QY 7 SFLDPLAGAAVAASVKTAVAPIERVYKLLQVQ-HASQISAQYKGIIDCVIRPEQ 65
 DB 7 NFMVDFLAGGSAASVKTAAPIERVKLLIQNDQMIRGLASPYKIGECFVRYRIDE 145
 QY 66 GFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFGVDRHKQWRYPAGNLASGAAGA 125
 DB 146 GFLSLMGNLANVIRYPTQALNFAFKDKYKQLFGVDRHKQWRYPAGNLASGAAGA 204
 QY 126 TSLCFVPLDFAFRLADVGR---AOREFHGIDCTIKFKSDGRLGYQFNVSQ 182
 DB 205 SLSLFVYSLDYARFRLANDAKSAGKGGDQFNGLVYRRTIKSDGIAGLYRGFNISCV 264
 QY 183 IITRAYRGVYDTAK-----GMLPDPKNVHIFVSMIAQSVTAAGLSTPEPTVRRM 237
 DB 265 IIVYRGLYFGLYSIRKVVLTGNLQD---NFAFSLGWLITNGAGLASPYDITVRRM 320
 QY 238 MMSGRGADIMYGTVDWCRKIAKDEGAKAFKFGANSNVLRGGAFLVLYDEI----- 293
 DB 321 MMSGEA---VKYSSIDARQQLIKKGKPSLFRGAGANILRAVAGVLAGYDQLQILF 377

Qy 294 --KXY 296
 Db 378 FGKXY 382

RESULT 15
 ADT_SCHPO STANDARD; PRT; 322 AA.
 AC Q09188;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ADP, ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).
 GN ANCL OR SPBC530.10C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 NCBI TaxID=4896;
 RX SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA MEDLINE=96257204; PubMed=8675018;
 RA Couzin N., Trezeguet V., Saux A.L., Lauguin G.J.M.;
 RT "Cloning of the gene encoding the mitochondrial adenine nucleotide carrier of Schizosaccharomyces pombe by functional complementation in Saccharomyces cerevisiae."
 RT Gene 171:113-117(1996).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=972;
 RC MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rejandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Scourse J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean C.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Gromprez B.,
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Pritz C., Holzer E., Moestl D., Hilbert H.,
 RA Botzys K., Langer I., Beck A., Leinrich H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe."
 RL Nature 415:871-880(2002).
 RL -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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 CC -----
 CC EMBL; 249974; CA90275.1; -
 CC EMBL; AL023634; CA19176.1; -
 CC PIR; T40526; T40526.
 CC Genedb_Spombe; SPBC530.10C; -
 CC InterPro; IPR002067; Mito_carrier.
 CC InterPro; IPR001993; Mitoch_carrier.
 CC Pfam; PF00153; mto_carri; 3.
 CC PRINTS; PR00926; MITOCARRIER.
 CC PROSITE; PS00215; MITOCH_CARRIER; 2.
 CC Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 28 48 1 (POTENTIAL).
 FT TRANSMEM 93 111 2 (POTENTIAL).
 FT TRANSMEM 131 151 3 (POTENTIAL).
 FT TRANSMEM 197 217 4 (POTENTIAL).
 FT TRANSMEM 222 242 5 (POTENTIAL).
 FT TRANSMEM 289 309 6 (POTENTIAL).
 SQ SEQUENCE 322 AA; 35020 MW; 8AC3D16A40F41AFC CRC64;
 Query Match 48.5%; Score 752.5; DB 1; Length 322;
 Best Local Similarity 52.9%; Pred. No. 4,4e-60;
 Matches 156; Conservative 51; Mismatches 75; Indels 13; Gaps 6;
 Qy 7 SFLKDLPLAGAAVAAVSTAVAPIRVYKLLQVQASKOISAEK--QYKGIIDCVVRIPK 63
 Db 26 TFFPDPFMVGGVSAVSTKTAAPIRVYKLLIQNQ--DEMIRAGRLSHRYKGGECFKRYA 83
 Qy 64 RQGLSPFRGNLANVIRYPPQALNPAFKDKYKQLPLFGVDRHROFWRYPAGNLASGGA 123
 Db 84 BEGVISLNRGNTAVLVIRFPQALNPAFKDKYKQLPLFGVDRHROFWRYPAGNLASGGA 142
 Qy 124 GATSLCEVYPLDFAETRLAAD--VGRRAQREHGLDPCIIRKSDGLRGLYOGFNVSV 180
 Db 143 GAASLLFVYSLDARTRLANDAKSAGKGGEGFGLVDVYKTRSDGLRGLYOGFNSV 202
 Qy 181 QGIIIRYPAIFGVYDIAKG-MLPDPKQVHIFVSMIAOSTAVAVGLLSYPTDYRRMM 239
 Db 203 VGIIVYRGLYFGMDTKPVVLVGLPGLNPLASFLGLMAVVTGSGVASYPLDTRRRMM 262
 Qy 240 QSGRKGADIVTGVDCMRKIANDEGAKPFKGSNVTLRGMGAFVLYVDEIK 294
 Db 263 TSGEA--VKYSSFEQGLAKESGKSPFKGAGNVLKGVAGVLSITDQV 314

Search completed: December 18, 2003, 12:41:23
 Job time : 9.31467 secs

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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:37:01 / Search time 30.598 Seconds
(without alignments)
2504.793 Million cell updates/sec

Title: US-09-811-131-31
Perfect score: 1553
Sequence: 1 MGDHANSFLDPLAGAVAA.....LRGNGAFVLVDIKKYV 297

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1464.5	94.3	298	6	O46373
2	1462.5	94.2	298	11	O8BVI9
3	1411.5	90.9	298	6	O8SOH5
4	1392.5	89.7	298	13	O8AYM3
5	1377.5	88.7	298	13	O9YIC4
6	1377.5	88.7	298	13	O9PWH1
7	1375.5	88.6	298	13	O8UHI0
8	1374.5	88.5	298	13	O9PRH2
9	1366.5	88.0	298	13	O919M9
10	1245.5	80.2	299	5	O95VX4
11	1241.5	79.9	300	5	O9NHW5
12	1241.5	79.9	312	5	O8IRAO
13	1234.5	79.5	317	13	O91336
14	1183	76.2	288	5	O44094
15	1183	76.2	288	5	O44093
16	1180.5	76.0	254	11	O8BKQ5

17	1147	73.9	307	5	O62526	O62526 drosophila
18	1139.5	73.4	304	5	O25129	O25129 halocynthia
19	1101.5	70.9	315	4	O9HOC2	O9HOC2 homo sapien
20	1045.5	67.3	313	5	P91410	P91410 caenorhabdi
21	1043.5	67.2	313	5	O21103	O21103 caenorhabdi
22	1042	67.1	310	10	O8H727	O8H727 phytophthor
23	1037.5	66.8	300	5	O45865	O45865 caenorhabdi
24	1005.5	64.7	300	5	O01813	O01813 caenorhabdi
25	993.5	64.0	300	5	O17407	O17407 caenorhabdi
26	989.5	63.7	309	5	O97470	O97470 dictyosteli
27	959	61.8	307	8	O9XM22	O9XM22 ascaris suu
28	950	61.2	318	5	O9BJ36	O9BJ36 toxoplasma
29	926.5	59.7	301	5	O8MVR4	O8MVR4 euploies sp
30	916.5	59.0	308	5	O8MVR8	O8MVR8 nycotetherus
31	914.5	58.9	305	5	O8MVR7	O8MVR7 nycotetherus
32	913.5	58.8	306	5	O8MVR5	O8MVR5 nycotetherus
33	908.5	58.5	301	5	O81J34	O81J34 plasmodium
34	906.5	58.4	308	5	O8MVR6	O8MVR6 nycotetherus
35	905.5	58.3	301	5	O25692	O25692 plasmodium
36	904.5	58.2	301	5	O26006	O26006 plasmodium
37	841.5	54.2	170	6	O9X869	O9X869 bus scrofa
38	772	49.7	306	5	O18683	O18683 caenorhabdi
39	757.5	48.8	305	3	O9P8M1	O9P8M1 yarrowia li
40	750.5	48.3	307	5	O76286	O76286 trypanosoma
41	748.5	48.2	303	3	O74260	O74260 candida par
42	746.5	48.1	379	10	O49447	O49447 arabidopsis
43	745.5	48.0	326	5	P91270	P91270 caenorhabdi
44	743.5	47.9	307	5	O26697	O26697 trypanosoma
45	743	47.8	302	3	O8J0M2	O8J0M2 yarrowia li

ALIGNMENTS

RESULT 1

O46373 PRELIMINARY; PRT; 298 AA.

AC 01-JUN-1998 (TREMBLrel. 06, Created)

DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE ADP/ATP translocase.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

FN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Skeletal muscle;

RA Yamaguchi N., Kasai M.;

RT "Identification of a 30kDa calsequestrin-binding protein, which regulates calcium release from sarcoplasmic reticulum of rabbit skeletal muscle."

RT J. Biochem. 335:541-547 (1998).

RL -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

CC EMBL; AB009386; BA23777.1; -

DR InterPro; IPR001993; Mitoch_carrier.

DR InterPro; IPR002067; Mit_carrier.

DR InterPro; IPR002030; Mit_uncoupling.

DR Pfam; PF00153; mito_carr1.3.

DR PRINTS; PR00926; MITOCARRIER.

DR PRINTS; PR00784; MTUNCOUPLING.

DR PROSITE; PS00215; MITOCH_CARRIER; 3.

KW Membrane; Transmembrane; Transport.

SQ SEQUENCE 298 AA; 32901 MW; CAEA32C88164AD78 CRC64;

Query Match 94.3%; Score 1464.5; DB 6; Length 298;
Best Local Similarity 94.6%; Pred. No. 7.2e-129;
Matches 282; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

OY 1 MGDHANSFLDPLAGAVAAVSKTAAVPIERVLLLOVCHASKQISAEKQYKIIIDCVR 60
DB 1 MSDQALSLKDFLAGVAAVSKTAAVPIERVLLLOVCHASKQISAEKQYKIIIDCVR 60

QY 61 IPKEGFLSPFRGNLANVIRYPTQALNPAFKDKYKQFLGVDHKKQFWRYPAGNLASG 120
 DB 61 IPKEGFLSPFRGNLANVIRYPTQALNPAFKDKYKQFLGVDHKKQFWRYPAGNLASG 120
 QY 121 GAAGATSLCFYVPLDPARTRLAADVGR-RAQREHFGLDCCIIFKPSGLGLYOGFNV 179
 DB 121 GAAGATSLCFYVPLDPARTRLAADVGR-RAQREHFGLDCCIIFKPSGLGLYOGFNV 180
 QY 180 VGGIITVAAAYFGVYDTRAKGMLPDPKNVHIFVSMIAOSVTAVALGLSYPPDTPVRRMM 239
 DB 181 VGGIITVAAAYFGVYDTRAKGMLPDPKNVHIFVSMIAOSVTAVALGLSYPPDTPVRRMM 240
 QY 240 QSGRKGADIMYTGTVDCWRKIAKDEGAKAFKAGANSVLRGMAFVLVLYDEIKKY 297
 DB 241 QSGRKGADIMYTGTVDCWRKIAKDEGAKAFKAGANSVLRGMAFVLVLYDEIKKY 298

RESULT 2

QY 08BV19 PRELIMINARY; PRT; 298 AA.
 ID 08BV19
 AC 08BV19;
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Solute carrier family 25.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium.
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT Nature 420:563-573 (2002).
 RL EMBL; AK078077; BAC37117.1;
 DR EMBL; AK078077; BAC37117.1;
 SQ SEQUENCE 298 AA; 32904 MW; F94C89009836710B CRC64;

Query Match 94.2%; Score 1462.5; DB 11; Length 298;
 Best Local Similarity 94.0%; Pred. No. 1.1e-128;
 Matches 280; Conservative 10; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDAHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDCVYR 60
 DB 1 MGDAHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDCVYR 60
 QY 61 IPKEGFLSPFRGNLANVIRYPTQALNPAFKDKYKQFLGVDHKKQFWRYPAGNLASG 120
 DB 61 IPKEGFLSPFRGNLANVIRYPTQALNPAFKDKYKQFLGVDHKKQFWRYPAGNLASG 120
 QY 121 GAAGATSLCFYVPLDPARTRLAADVGR-RAQREHFGLDCCIIFKPSGLGLYOGFNV 179
 DB 121 GAAGATSLCFYVPLDPARTRLAADVGR-RAQREHFGLDCCIIFKPSGLGLYOGFNV 180
 QY 180 VGGIITVAAAYFGVYDTRAKGMLPDPKNVHIFVSMIAOSVTAVALGLSYPPDTPVRRMM 239
 DB 181 VGGIITVAAAYFGVYDTRAKGMLPDPKNVHIFVSMIAOSVTAVALGLSYPPDTPVRRMM 240
 QY 240 QSGRKGADIMYTGTVDCWRKIAKDEGAKAFKAGANSVLRGMAFVLVLYDEIKKY 297
 DB 241 QSGRKGADIMYTGTVDCWRKIAKDEGAKAFKAGANSVLRGMAFVLVLYDEIKKY 298

RESULT 3

QY 08SOH5 PRELIMINARY; PRT; 298 AA.
 ID 08SOH5
 AC 08SOH5;
 DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)

DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Adenine nucleotide translocator 2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NC NCB1_TaxID=9913;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Yamazaki N., Shinohara Y., Tanida K., Terada H.;
 RT "Structural properties of mammalian mitochondrial ADP/ATP carriers:
 RT identification of possible amino acids that determine functional
 RT differences in its isoforms."
 RL Mitochondrion 1:371-379 (2002).
 DR EMBL; AB065433; BAB84673.1;
 DR Interpro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 SQ SEQUENCE 298 AA; 32955 MW; CB6897B987B79C0 CRC64;

Query Match 90.9%; Score 1411.5; DB 6; Length 298;
 Best Local Similarity 89.9%; Pred. No. 6.6e-124;
 Matches 267; Conservative 16; Mismatches 13; Indels 1; Gaps 1;

QY 1 MGDAHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDCVYR 60
 DB 1 MTDAVSPADKDFLAGAANAASKTAVAPIERVKLLQVQHASKQITADKQYKGIIDCVYR 60
 QY 61 IPKEGFLSPFRGNLANVIRYPTQALNPAFKDKYKQFLGVDHKKQFWRYPAGNLASG 120
 DB 61 IPKEGFLSPFRGNLANVIRYPTQALNPAFKDKYKQFLGVDHKKQFWRYPAGNLASG 120
 QY 121 GAAGATSLCFYVPLDPARTRLAADVGR-RAQREHFGLDCCIIFKPSGLGLYOGFNV 179
 DB 121 GAAGATSLCFYVPLDPARTRLAADVGR-RAQREHFGLDCCIIFKPSGLGLYOGFNV 180
 QY 180 VGGIITVAAAYFGVYDTRAKGMLPDPKNVHIFVSMIAOSVTAVALGLSYPPDTPVRRMM 239
 DB 181 VGGIITVAAAYFGVYDTRAKGMLPDPKNVHIFVSMIAOSVTAVALGLSYPPDTPVRRMM 240
 QY 240 QSGRKGADIMYTGTVDCWRKIAKDEGAKAFKAGANSVLRGMAFVLVLYDEIKKY 296
 DB 241 QSGRKGADIMYTGTVDCWRKIAKDEGAKAFKAGANSVLRGMAFVLVLYDEIKKY 297

RESULT 4

QY 08AVM3 PRELIMINARY; PRT; 298 AA.
 ID 08AVM3
 AC 08AVM3;
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE ATP/ADP antiporter.
 GN AVANT.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NC NCB1_TaxID=9931;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Toyomizu M., Ueda M., Sato S., Seki Y., Sato K., Akiba Y.;
 RT "Cold-induced mitochondrial uncoupling and expression of chicken UCP
 RT and ANT mRNA in chicken skeletal muscle."
 RL FEBS Lett. 0:0-0 (2002).
 DR EMBL; AB088686; BAC15533.1;
 SQ SEQUENCE 298 AA; 32847 MW; 1174CC5E400A10D CRC64;

Query Match 89.7%; Score 1392.5; DB 13; Length 298;
 Best Local Similarity 88.3%; Pred. No. 4e-122;
 Matches 263; Conservative 18; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDAHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDCVYR 60

Query Match	88.6%;	Score 1375.5;	DB 13;	Length 298;
Best Local Similarity	86.9%;	Pred. No. 1.6e-120;		
Matches 259;	Conservative 22;	Mismatches 16;	Indels 1;	Gaps 1;

RESULT 8	
Q9PRH2	
ID Q9PRH2	PRELIMINARY;
	PRT; 298 AA

EMBL; AB008459; BAA36509.1; -..

QY 1 MGHAMSEFKDPLAGVAAVAASKTVAPLERVKLLQYHASKQISAEKQYKGIIDCVAR 60

Db 1 MTPAAISPAKDFLAGVAAAIKSTVAPLERVKLLQYHASKQITADQYKGIIDCVAR 60

RESULT 9
Q919M9
ID Q919M9 PRELIMINARY; PRT; 298 AA

DR InterPro; IPR002067; Mlt_carrier.
DR InterPro; IPR002030; Mlt_uncoupling
Pfam; PF00153; mlt_carr; 3.
DR

Query Match	88.0%	Score 1366.5;	DB 13;	Length 298;
Best Local Similarity	86.2%	Pred. No. 1.le-119;		
Matches 257; Conservative	23;	Mismatches 17;	Indels 1;	Gaps 1;

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01 1 MGDHMSFLKDFLAGVAVAASKTAVAPIERVKLLQVQHASKQJSAEKQYKGIIDCVR 600
02

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Db 1 MTDAAISPAKDFLAGVAAAIKTAIVAPIERVKLLQVOHASKOITADKHYKIMDCVVR 60
 Qy 61 IPKOGFLSPWGNLANVIRFPYQALNPAFKDKYKOLFLGVDVHRKQFMRYPAGNLASG 120
 Db 61 IPKOGFLSPWGNLANVIRFPYQALNPAFKDKYKOLFLGVDVHRKQFMRYPAGNLASG 120
 Qy 121 GAAGATSLCFYYPPLDPARTRLAADVGRRA-OREFHGLDGCIIKIFKSDGLRGLYOGFNVS 179
 Db 121 GAAGATSLCFYYPPLDPARTRLAADVGRRA-OREFHGLDGCIIKIFKSDGLRGLYOGFNVS 180
 Qy 180 VQGIITRYAAVFGYVDIAKGMPLDPKXNVHIFVSMIAOSVTAVALGLSYPPDYVRRMM 239
 Db 181 VQGIITRYAAVFGYVDIAKGMPLDPKXNVHIFVSMIAQTVTAVALGASYPDYVRRMM 240
 Qy 240 QSGRKGADIMYGVDCWRKIAKDEGAAFFKGSANVLRMGCAFVLYVDEIKKYV 297
 Db 241 QSGRKGADIMYGVDCWRKIAKDEGAAFFKGSANVLRMGCAFVLYVDEIKKYV 298

RESULT 10

Q95VX4 PRELIMINARY; PRT; 299 AA.
 ID Q95VX4
 AC Q95VX4
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE ADP-ATP translocator.
 OS Bthmoticigmus rubripes.
 OC Eukaryota; Metazoa; Arthropoda; Myriapoda; Chilopoda;
 OC Pleurostigmophora; Scolopendromorpha; Scolopendridae; Bthmoticigmus.
 NCBI_TaxID=62613;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Burnell J.N.;
 RT "Nucleotide sequence of an ADP-ATP translocator of Bthmoticigmus rubripes."
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF401758; AAL02100.1; -
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR02067; Mit_carrier.
 DR Pfam; PF00153; mito_carrt; 3.
 DR PRINTS; PRO0926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 SQ SEQUENCE 299 AA; 33037 MM; 3C3BGB2SE7C3CE CRC64;

Query Match 80.2%; Score 1245.5; DB 5; Length 299;
 Best Local Similarity 80.3%; Pred. No. 2.3e-108;
 Matches 236; Conservative 25; Mismatches 32; Indels 1; Gaps 1;

Qy 5 AMSFLKDFLAGVAAAVSKTAVAPIERVKLLQVOHASKOISAKOKYKGIIDCVVRIPKE 64
 Db 5 AMSFLKDFLAGVAAAVSKTAVAPIERVKLLQVOHASKOISAKOKYKGIIDCVVRIPKE 64
 Qy 65 QGFLSPWGNLANVIRFPYQALNPAFKDKYKOLFLGVDVHRKQFMRYPAGNLASG 124
 Db 65 QGFLSPWGNLANVIRFPYQALNPAFKDKYKOLFLGVDVHRKQFMRYPAGNLASG 124
 Qy 125 ATSLCFYYPPLDPARTRLAADVGR-RAOREFHGLDGCIIKIFKSDGLRGLYOGFNVS 183
 Db 125 ATSLCFYYPPLDPARTRLAADVGR-RAOREFHGLDGCIIKIFKSDGLRGLYOGFNVS 184
 Qy 184 IITYAAVFGYVDIAKGMPLDPKXNVHIFVSMIAOSVTAVALGLSYPPDYVRRMM 243
 Db 185 IITYAAVFGYVDIAKGMPLDPKXNVHIFVSMIAQTVTAVALGASYPDYVRRMM 244
 Qy 244 KGADIMYGVDCWRKIAKDEGAAFFKGSANVLRMGCAFVLYVDEIKKYV 297
 Db 245 KGADIMYGVDCWRKIAKDEGAAFFKGSANVLRMGCAFVLYVDEIKKYV 298

RESULT 11
 Q9NHW5 PRELIMINARY; PRT; 300 AA.

AC Q9NHW5;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE ADP-ATP translocator.
 OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Lucilia.
 NCBI_TaxID=7375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=SS mal seeking;
 RC Chen Z., Pair J.A., Batterham P.;
 RT "A cDNA clone encoding the ADP-ATP translocase of Lucilia cuprina."
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
 CC -1-SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AF218587; AF32322.1; -
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR02067; Mit_carrier.
 DR Pfam; PF00153; mito_carrt; 3.
 DR PRINTS; PRO0926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Membrane; Transmembrane; Transport.
 SQ SEQUENCE 300 AA; 33036 MM; 5459DFOEA0E2E742 CRC64;

Query Match 79.9%; Score 1241.5; DB 5; Length 300;
 Best Local Similarity 78.7%; Pred. No. 5.6e-108;
 Matches 236; Conservative 25; Mismatches 36; Indels 3; Gaps 1;

Qy 1 MGDA---WSFLKDFLAGVAAAVSKTAVAPIERVKLLQVOHASKOISAKOKYKGIIDC 57
 Db 1 MGDAADPLGVDFVDFALGSAVSKTAVAPIERVKLLQVOHASKOISAKOKYKGIIDC 60
 Qy 58 VVRIPKOGFLSPWGNLANVIRFPYQALNPAFKDKYKOLFLGVDVHRKQFMRYPAGNL 117
 Db 61 FVRIPKOGFLSPWGNLANVIRFPYQALNPAFKDKYKOLFLGVDVHRKQFMRYPAGNL 120
 Qy 118 ASGAAGATSLCFYYPPLDPARTRLAADVGRRAOREFHGLDGCIIKIFKSDGLRGLYOGFN 177
 Db 121 ASGAAGATSLCFYYPPLDPARTRLAADVGRRAOREFHGLDGCIIKIFKSDGLRGLYOGFN 180
 Qy 178 VSVQGIITRYAAVFGYVDIAKGMPLDPKXNVHIFVSMIAOSVTAVALGLSYPPDYVRRM 237
 Db 181 VSVQGIITRYAAVFGYVDIAKGMPLDPKXNVHIFVSMIAQTVTAVALGASYPDYVRRM 240
 Qy 238 MMSGKRGADIMYGVDCWRKIAKDEGAAFFKGSANVLRMGCAFVLYVDEIKKYV 297
 Db 241 MMSGKRGADIMYGVDCWRKIAKDEGAAFFKGSANVLRMGCAFVLYVDEIKKYV 300

RESULT 12

Q8IRAO PRELIMINARY; PRT; 312 AA.
 ID Q8IRAO
 AC Q8IRAO
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE CG16944-PC.
 GN SRSB.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=2019606; PubMed=10731132;
 RA Adams W.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abell J.F., Agbayan A., An H.J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Bendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Butkova D., Botchan M.R., Butler H., Brodstein P., Brodter P.,
 RA Buttle K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Dublin K.Y., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glaeser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Houston D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B., Kodish C., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Metkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacle J.M.,
 RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kimmo I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodard, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Sequence 287:2185-2195(2000).

[2]
 RP SEQUENCE FROM N.A.
 RA Ceinlier S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amaratunga P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banzon K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dorsett K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferreira S., Frise E., Galle R.F., Gary N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Houston D., Howland T.J.,
 RA Ibegwam C., Jatali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacle J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Peltman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of Drosophila melanogaster genome.";
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.

[3]
 RP SEQUENCE FROM N.A.
 RA Mirra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecny P., Huang X., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Rudy J.L., Bergman C., Berman B., Carlson J.W., Ceinlier S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Seale S.M.J., Smith R., Shu S., Smutnick J., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.B.;
 RT "Annotation of Drosophila melanogaster genome.";
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.

[4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Ceinlier S.E., Gibbs R.A., Rubin G.M., Venter J.C.;
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AE003484; AA002671; -;
 SQ SEQUENCE 312 AA; 34214 MW; 78D5834E74E168DF CRC64;

Query Match 79.9%; Score 1241; DB 5; Length 312;

Best Local Similarity 79.7%; Pred. No. 6-66-108;
 Matches 232; Conservative 26; Mismatches 33; Indels 0; Gaps 0;
 QY 5 AMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYKIIDCVRIPE 64
 DB 20 AVGVQKDPADAGISAAVSKTAVAPIERVKLLQVQHASKOISAEKQYKIIDCVRIPE 79
 QY 65 QGFLSPFRGNLANVIRFPPTALNPAFKDKKQFLGVDVHKKQFWRFPAGNLASGGAAG 124
 DB 80 QGFSFPRGNLANVIRFPPTALNPAFKDKKQFLGVDVHKKQFWRFPAGNLASGGAAG 139
 QY 125 ATSLCFVPLDPARTLADVGRBROREPHGLGDCIIRIFPSDGLRGLYOGFNVSVGII 184
 DB 140 ATSLCFVPLDPARTLADVGRBROREPHGLGDCIIRIFPSDGLRGLYOGFNVSVGII 199
 QY 185 IYRAAYFGVDTAKGMLPDPKNVHIFVSWMIQSVTAVAGLLSYFPDTRRRMMQSGRK 244
 DB 200 IYRAAYFGVDTAKGMLPDPKNVHIFVSWMIQSVTAVAGLLSYFPDTRRRMMQSGRK 259
 QY 245 GADIMTGTVDCKRIADBGAKAFPKGAWSNVIRGAGAVLVLYDEIKK 295
 DB 260 ATEYIKNTLHCWNTIAKQEGTGAFPKGAFSNILRGTAFLVLYDEIKK 310

RESULT 13

QY 091336 PRELIMINARY; PRT; 317 AA.
 ID 091336
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE ADP/ATP translocase.
 OS Rana sylvatica (Wood frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
 OX NCBI_TaxId=45436;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=97398141; PubMed=9256066;
 RA Cal O., Greenway S.C., Storey K.B.;
 RT "Differential regulation of the mitochondrial ADP/ATP translocase gene
 in wood frogs under freezing stress.";
 RL Biochim. Biophys. Acta 1353:65-76(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Cal O., Storey K.B.;
 RL Submitted (APR-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; U4832; AA97882.2; -;
 DR InterPro; IPR001993; Mitoch. carrier.
 DR InterPro; IPR002067; Mit. carrier.
 DR Pfam; PF00153; mito. carri. 3.
 DR PRINTS; PR00926; MITOCHARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Membrane; Transmembrane; Transport.
 SQ SEQUENCE 317 AA; 35005 MW; 5F6687ED85CEB72 CRC64;

Query Match 79.5%; Score 1234.5; DB 13; Length 317;
 Best Local Similarity 85.7%; Pred. No. 2-76-107;
 Matches 233; Conservative 21; Mismatches 17; Indels 1; Gaps 1;

QY 1 MGDHAWFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEKQYKIIDCVRIPE 60
 DB 1 MTDAAASFADDFLAGAANAASKTAVAPIERVKLLQVQHASKOITADKQKGLMDCVRIPE 60
 QY 61 IPKQGFSPFRGNLANVIRFPPTALNPAFKDKKQFLGVDVHKKQFWRFPAGNLASG 120
 DB 61 IPKQGFSPFRGNLANVIRFPPTALNPAFKDKKQFLGVDVHKKQFWRFPAGNLASG 120
 QY 121 GAAGTSLCFVPLDPARTLADVGRBROREPHGLGDCIIRIFPSDGLRGLYOGFNVSVGII 179

Db 121 GAAGATSLCFYVPLDPFARTRLAADVGKAGREENGGLDCLAKIFKSDGLKGLYQGFVNS 180
 QY 180 VGGIITRAAAYGVYDTAKGLPDPKXNHIFVSWMIASQVAVAGLLSPEDTVRRMM 239
 Db 181 VGGIITRAAAYGVYDTAKGLPDPKXNHIFVSWMIASQVAVAGFGSPEDTVRRMM 240
 QY 240 QSGRKGADIMYTGWDCKRIKADGAKAFK 271
 Db 241 QSGRKGADIMYTGWDCKRIKADGAKAFK 272

RESULT 14

044094

PRELIMINARY; PRT; 288 AA.

AC 044094
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE ADP/ATP translocase (Fragment).
 GN SSB.
 OS Drosophila subobscura (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7241;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;
 RL Genetics 0:0-0(1997).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AF025799; AAB87884.1; -;
 DR FLYBase; FBgn0023237; Dsub\seeb.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mlt_carrier.
 DR Pfam; PF00153; mltc_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Membrane; Repeat; Transmembrane; Transport.
 FT NON TER 288
 SQ SEQUENCE 288 AA; 31775 MW; 06A1D1E477B81B26 CRC64;

Query Match 76.2%; Score 1183; DB 5; Length 288;
 Best Local Similarity 79.6%; Pred. No. 1.6e-102;
 Matches 226; Conservative 23; Mismatches 33; Indels 2; Gaps 2;

QY 5 AWSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDCVRIPE 64
 Db 7 AIGFVKDFPFAAGGISAASKTAVAPIERVKLLQVQHSKQISPDQYKGMVDCFRIPKE 66
 QY 65 QGPISTFMRGNLANIRYPTQALNPAFKDKKQLFLGVDNHRKQFMRYPAGNLASGGAAG 124
 Db 67 QGFSSFWRGNLANIRYPTQALNPAFKDKKQVFLGVDNKTQFMRYPAGNLASGGAAG 126
 QY 125 ATSLCFYVPLDPFARTRLAADVGRRAREFHGLGDCIIRKPSDGLRGLYOGFNVSVGGII 184
 Db 127 ATSLCFYVPLDPFARTRLAADVGRRAREFHGLGDCIIRKPSDGLRGLYOGFNVSVGGII 186
 QY 185 IYRAAYFGVYDTAKGLPDPKXNHIFVSWMIASQVAVAGLLSPEDTVRRMMQSGRK 244
 Db 187 IYRAAYFGVYDTAKGLPDPKXNHIFVSWMIASQVAVAGLLSPEDTVRRMMQSGRK 245
 QY 245 GADIMYTGWDCKRIKADGAKAFKGMANSNVLKMGGAFLV 288
 Db 246 ATEIITYKNTLHCWGTIAKQEGT-AFFKGAFSNVLKGTGAFLV 288

RESULT 15

044093

PRELIMINARY; PRT; 288 AA.

AC 044093
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE ADP/ATP translocase (Fragment).
 GN SSB.
 OS Drosophila pseudoobscura (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7237;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;
 RL Genetics 0:0-0(1997).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AF025798; AAB87883.1; -;
 DR FLYBase; FBgn0023293; Dpse\seeb.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mlt_carrier.
 DR Pfam; PF00153; mltc_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Membrane; Repeat; Transmembrane; Transport.
 FT NON TER 288
 SQ SEQUENCE 288 AA; 31725 MW; 052B0CC0050436B0 CRC64;

Query Match 76.2%; Score 1183; DB 5; Length 288;
 Best Local Similarity 79.6%; Pred. No. 1.6e-102;
 Matches 226; Conservative 25; Mismatches 31; Indels 2; Gaps 2;

QY 5 AWSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDCVRIPE 64
 Db 7 AIGFVKDFPFAAGGISAASKTAVAPIERVKLLQVQHSKQISPDQYKGMVDCFRIPKE 66
 QY 65 QGPISTFMRGNLANIRYPTQALNPAFKDKKQLFLGVDNHRKQFMRYPAGNLASGGAAG 124
 Db 67 QGFSSFWRGNLANIRYPTQALNPAFKDKKQVFLGVDNKTQFMRYPAGNLASGGAAG 126
 QY 125 ATSLCFYVPLDPFARTRLAADVGRRAREFHGLGDCIIRKPSDGLRGLYOGFNVSVGGII 184
 Db 127 ATSLCFYVPLDPFARTRLAADVGRRAREFHGLGDCIIRKPSDGLRGLYOGFNVSVGGII 186
 QY 185 IYRAAYFGVYDTAKGLPDPKXNHIFVSWMIASQVAVAGLLSPEDTVRRMMQSGRK 244
 Db 187 IYRAAYFGVYDTAKGLPDPKXNHIFVSWMIASQVAVAGLLSPEDTVRRMMQSGRK 245
 QY 245 GADIMYTGWDCKRIKADGAKAFKGMANSNVLKMGGAFLV 288
 Db 246 ATEIITYKNTLHCWGTIAKQEGT-AFFKGAFSNVLKGTGAFLV 288

Search completed: December 18, 2003, 12:43:09
 Job time : 32.598 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:34:56 ; Search time 35.3729 Seconds
(without alignments)
1337.197 Million cell updates/sec

Title: US-09-811-131-32

Sequence: 1 MTDAALSAKDFLAGVAA.....LRNGCAFLVLYDEIKYT 298

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1547	100.0	298	AAV71032	Human adenine nucl
2	1547	100.0	298	AAU01199	Human adenine nucl
3	1547	100.0	298	AAU10379	Human adenine nucl
4	1537	99.4	298	AAO18516	Human insulin rece
5	1454	94.0	298	AAV71033	Human adenine nucl
6	1454	94.0	298	AAAM39641	Human polypeptide
7	1454	94.0	298	AAU01200	Human adenine nucl
8	1454	94.0	298	AAU10380	Human adenine nucl
9	1454	94.0	323	AAAM41427	Human polypeptide

10	1417	91.6	325	22	ABG15423
11	1411	91.2	298	19	AAAG61169
12	1409	91.1	293	22	ABU53219
13	1391.5	89.9	297	21	AAV71031
14	1391.5	89.9	297	23	AAU01198
15	1391.5	89.9	297	23	AAU10378
16	1346	87.0	263	23	ABG27056
17	1339	86.6	429	24	ABR41715
18	1253.5	81.0	299	22	ABBE6082
19	1253.5	81.0	299	22	ABBE7300
20	1125.5	72.8	307	22	ABBS8380
21	1102	71.2	315	23	ABU53218
22	1102	71.2	315	23	ABR21175
23	988	63.9	228	23	ABP43205
24	923	59.7	222	23	ABP74105
25	895.5	57.9	298	22	ABG18922
26	792	51.2	484	22	ABG15422
27	792	51.2	484	22	ABG27055
28	779.5	50.4	301	23	ABP73357
29	747.5	48.3	346	21	AAAG36577
30	747.5	48.3	346	21	AAAG37261
31	747.5	48.3	346	21	AAAG37264
32	747.5	48.3	346	21	AAAG37264
33	747.5	48.3	363	21	AAAG36576
34	747.5	48.3	363	21	AAAG37260
35	747.5	48.3	363	21	AAAG37263
36	747.5	48.3	363	21	AAAG38459
37	747.5	48.3	381	21	AAAG36575
38	747.5	48.3	381	21	AAAG37259
39	747.5	48.3	381	21	AAAG37262
40	747.5	48.3	381	21	AAAG38458
41	747.5	48.3	992	21	AAAG38672
42	747.5	48.3	1009	21	AAAG38671
43	747.5	48.3	1027	21	AAAG38671
44	746	48.2	379	24	ABP81267
45	744.5	48.1	346	21	AAAG17731

ALIGNMENTS

RESULT 1	AAV71032	standard; Protein; 298 AA.
ID	AAV71032	
AC	AAV71032;	
DT	29-AUG-2000	(first entry)
DE	Human adenine nucleotide translocator ANT2.	
XX	Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP;	
XX	adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;	
XX	mitochondrial permeability transition; neuroprotective; neurotrophic;	
XX	antiparkinsonian; cytotatic; antidiabetic; anticonvulsant; neurolytic;	
XX	antiprotic; cerebroprotective; therapeutic; screening; poriasis;	
XX	Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;	
XX	diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;	
XX	mitochondrial encephalopathy; lactic acidosis; stroke; MTD;	
XX	mitochondrial diabetes and deafness; hyperproliferative disorder;	
XX	myoclonic epilepsy red ragged fibre syndrome.	
OS	Homo sapiens.	
PN	WO200026370-A2.	
PD	11-MAY-2000.	
XX		
PF	03-NOV-1999;	99WO-US25883.
XX		
PR	03-NOV-1998;	98US-0185904.
XX	08-SEP-1999;	99US-0393441.
XX		

PA (MITO-) MITOKOR.
 XX
 XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR,
 PI Ghosh SS,
 XX MPI; 2000-365619/31.
 DR N-PSDB; AAD00520.
 XX
 XX Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 XX
 XX Claim 45; Page 172-173; 175pp; English.
 XX
 XX The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT2 from human brain.
 XX
 XX Sequence 298 AA;
 SQ
 Query Match 100.0%; Score 1547; DB 21; Length 298;
 Best Local Similarity 100.0%; Pred. No. 2.3e-154;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTDAALSPAKDFLAGGVAASAKTAVAPIERVKLLQVQHASKOITADKOYKGIIDCVVR 60
 DB 1 MTDAALSPAKDFLAGGVAASAKTAVAPIERVKLLQVQHASKOITADKOYKGIIDCVVR 60
 QY 61 IPKQEVLSFWRGNLANVIRYFPQALNFAFKDKTKYKQIFLGVDKRTQFWRYFAGNLASG 120
 DB 61 IPKQEVLSFWRGNLANVIRYFPQALNFAFKDKTKYKQIFLGVDKRTQFWRYFAGNLASG 120
 QY 61 IPKQEVLSFWRGNLANVIRYFPQALNFAFKDKTKYKQIFLGVDKRTQFWRYFAGNLASG 120
 DB 61 IPKQEVLSFWRGNLANVIRYFPQALNFAFKDKTKYKQIFLGVDKRTQFWRYFAGNLASG 120
 QY 121 GAAGATSLCFYYPIDFARTRLAADVGKAGARERFGDCLVKIKSGIKGLVQGFNVAS 180
 DB 121 GAAGATSLCFYYPIDFARTRLAADVGKAGARERFGDCLVKIKSGIKGLVQGFNVAS 180
 QY 181 VGGIITRAAYFGIYDPAKGMPLDPKNTHTIVSNMIAQTVAVAGLTSYPEDTVRRMM 240
 DB 181 VGGIITRAAYFGIYDPAKGMPLDPKNTHTIVSNMIAQTVAVAGLTSYPEDTVRRMM 240
 QY 241 QSGRKGTDIMYTGTLDCWRKIARDEGGKAFKFGKAMSNTLRMGAFVLVLDKIKYT 298
 DB 241 QSGRKGTDIMYTGTLDCWRKIARDEGGKAFKFGKAMSNTLRMGAFVLVLDKIKYT 298
 RESULT 2
 AAU01199
 ID AAU01199 standard; Protein; 298 AA.
 XX
 XX AAU01199;
 AC
 XX 07-SEP-2001 (first entry)
 DT
 XX
 XX Human adenine nucleotide translocator-2 (ANT-2) protein.
 DE
 XX Human; adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

XX
 OS Homo sapiens.
 XX
 XX WO200132876-A2.
 XX
 XX 10-MAY-2001.
 PD
 XX
 XX 03-NOV-2000; 2000WO-US30535.
 PF
 XX
 XX 03-NOV-1999; 99US-0434354.
 PR
 XX
 XX (MITO-) MITOKOR.
 PA
 XX
 XX Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG,
 PI Vellicelebi G, Davis RB,
 XX MPI; 2001-291054/30.
 DR N-PSDB; AAS05902.
 XX
 XX New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX
 XX Disclosure; Fig 2; 186pp; English.
 PS
 XX The present sequence represents human adenine nucleotide translocator-2
 CC (ANT-2) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLAISH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 CC
 XX Sequence 298 AA;
 SQ
 Query Match 100.0%; Score 1547; DB 22; Length 298;
 Best Local Similarity 100.0%; Pred. No. 2.3e-154;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTDAALSPAKDFLAGGVAASAKTAVAPIERVKLLQVQHASKOITADKOYKGIIDCVVR 60
 DB 1 MTDAALSPAKDFLAGGVAASAKTAVAPIERVKLLQVQHASKOITADKOYKGIIDCVVR 60
 QY 61 IPKQEVLSFWRGNLANVIRYFPQALNFAFKDKTKYKQIFLGVDKRTQFWRYFAGNLASG 120
 DB 61 IPKQEVLSFWRGNLANVIRYFPQALNFAFKDKTKYKQIFLGVDKRTQFWRYFAGNLASG 120
 QY 61 IPKQEVLSFWRGNLANVIRYFPQALNFAFKDKTKYKQIFLGVDKRTQFWRYFAGNLASG 120
 DB 61 IPKQEVLSFWRGNLANVIRYFPQALNFAFKDKTKYKQIFLGVDKRTQFWRYFAGNLASG 120
 QY 121 GAAGATSLCFYYPIDFARTRLAADVGKAGARERFGDCLVKIKSGIKGLVQGFNVAS 180
 DB 121 GAAGATSLCFYYPIDFARTRLAADVGKAGARERFGDCLVKIKSGIKGLVQGFNVAS 180
 QY 181 VGGIITRAAYFGIYDPAKGMPLDPKNTHTIVSNMIAQTVAVAGLTSYPEDTVRRMM 240
 DB 181 VGGIITRAAYFGIYDPAKGMPLDPKNTHTIVSNMIAQTVAVAGLTSYPEDTVRRMM 240
 QY 241 QSGRKGTDIMYTGTLDCWRKIARDEGGKAFKFGKAMSNTLRMGAFVLVLDKIKYT 298
 DB 241 QSGRKGTDIMYTGTLDCWRKIARDEGGKAFKFGKAMSNTLRMGAFVLVLDKIKYT 298

RESULT 3
AAU10379
ID AAU10379 standard; Protein; 298 AA.
XX
AC AAU10379;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human adenine nucleotide translocator 2 (ANT2).
XX
KM Human; adenine nucleotide translocator; ANT; SB;
KW mitochondrial matrix protein.
XX
OS Homo sapiens.
XX
PN WO200185944-A2.
XX
PD 15-NOV-2001.
XX
PF 11-MAY-2001; 2001WO-US15416.
XX
PR 11-MAY-2000; 2000US-0569327.
XX
PS (MITO-) MITOKOR.
XX
PI Anderson CM, Davis RE, Clevenger W, Wiley SB, Miller SW, Szabo TR;
PI Ghosh SS, Moos WH, Pei Y, Carroll AK;
DR WPI; 2002-055598/07.
DR N-PSDB; AAS16689.
XX
PT Novel recombinant expression construct for producing adenine nucleotide
PT translocator polypeptides, comprises a regulated promoter linked to
PT nucleic acid encoding the polypeptide
XX
PS Claim 44; Fig 2; 147pp; English.
XX
CC The invention relates to a recombinant expression construct (I)
CC comprising a regulated promoter operably linked to a nucleic acid
CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
CC proteins mediate the exchange of ATP synthesized in the mitochondrial
CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
CC culturing the host cell. (I) is also useful for targeting a polypeptide
CC of interest to a mitochondrial membrane, where ANT polypeptide is
CC expressed as a fusion protein with the polypeptide of interest.
CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
CC useful for identifying an agent that binds to an ANT polypeptide. ANT
CC ligand is useful for determining the presence of an ANT polypeptide,
CC ANT from a biological sample, where the ANT ligand is covalently or non-
CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
CC useful for identifying an agent that interacts with an ANT polypeptide.
CC The present sequence represents the amino acid sequence of human ANT2.
XX
SQ Sequence 298 AA;
Query Match 100.0%; Score 1547; DB 23; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.3e-154;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTDAALSPADPFLAGVAAASKTAAPVPIERVKLLDVOHASKQITADKQYKGIIDCVNR 60
DB 1 MTDAALSPADPFLAGVAAASKTAAPVPIERVKLLDVOHASKQITADKQYKGIIDCVNR 60
QY 61 IPKQEVLSFWRGNLANVIRYFPQALNFAFKDKYKQIFLGVDVKRTQFWRYPFAGNLASG 120
DB 61 IPKQEVLSFWRGNLANVIRYFPQALNFAFKDKYKQIFLGVDVKRTQFWRYPFAGNLASG 120
QY 121 GAAGATSLCFYRPLDFAFTRILAAVGVGAERERFGADCLVKTKSDGKIGLYQGFNVIS 180
DB 121 GAAGATSLCFYRPLDFAFTRILAAVGVGAERERFGADCLVKTKSDGKIGLYQGFNVIS 180

QY 181 VQGIITRYAAVFGIYDPAKGLPDPKNTHTIVISWMIQTVTAAGLTSPEDTVRRMM 240
DB 181 VQGIITRYAAVFGIYDPAKGLPDPKNTHTIVISWMIQTVTAAGLTSPEDTVRRMM 240
QY 241 QSGRKGTDIMYTGLDCCWRKIARDDEGKAPFKGAMSNVLKMGAPVLVIYDEIKKTT 298
DB 241 QSGRKGTDIMYTGLDCCWRKIARDDEGKAPFKGAMSNVLKMGAPVLVIYDEIKKTT 298
RESULT 4
AAO18516
ID AAO18516 standard; Protein; 298 AA.
XX
AC AAO18516;
XX
DT 11-OCT-2002 (first entry)
XX
DE Human insulin receptor signaling modifier SEQ ID NO: 54.
XX
KM Human; insulin receptor signaling; insulin receptor signaling modifier;
KW ISM; diabetes; metabolic syndrome; antidiabetic.
XX
OS Homo sapiens.
XX
PN WO200255664-A2.
XX
PD 18-JUL-2002.
XX
PF 11-JAN-2002; 2002WO-US01048.
XX
PR 12-JAN-2001; 2001US-261226P.
PR 12-JAN-2001; 2001US-261303P.
PR 12-JAN-2001; 2001US-261304P.
PR 12-JAN-2001; 2001US-261335P.
PR 12-JAN-2001; 2001US-261336P.
PR 12-JAN-2001; 2001US-261361P.
PR 12-JAN-2001; 2001US-261457P.
PR 12-JAN-2001; 2001US-261458P.
PR 12-JAN-2001; 2001US-261459P.
PR 12-JAN-2001; 2001US-261461P.
PR 12-JAN-2001; 2001US-261518P.
PR 12-JAN-2001; 2001US-261531P.
PR 12-JAN-2001; 2001US-261532P.
PR 12-JAN-2001; 2001US-261533P.
PR 12-JAN-2001; 2001US-261589P.
PR 12-JAN-2001; 2001US-261590P.
PR 12-JAN-2001; 2001US-261694P.
PR 12-JAN-2001; 2001US-261695P.
PR 12-JAN-2001; 2001US-261697P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Seidel-Dugan C, Ferguson KC, Kidd T;
PI WPI; 2002-599664/64.
DR N-PSDB; AAL48635.
XX
PT Identifying an insulin receptor signaling modulator, useful as drug
PT targets for treating diabetes or metabolic disorders, comprises
PT contacting an assay system comprising insulin receptor signaling
PT modifiers with a test agent
XX
PS Disclosure; Page 160-161, 232pp; English.
XX
CC The present invention relates to a method of identifying a candidate
CC insulin receptor (INR) signaling modulating agent, involving contacting
CC an assay system comprising an insulin receptor signaling modifier (ISM)
CC polypeptide or nucleic acid with a test agent, and detecting a test
CC agent-biased activity of the assay system. The method is useful for
CC identifying candidate INR signaling modulating agents. ISM genes may be
CC used as drug targets for treatment of disorders related to INR signaling
CC such as diabetes or metabolic syndrome. ISM nucleic acids and
CC polypeptides are useful for identifying and testing agents that modulate

CC ISM function and for other applications related to the involvement of ISM
 CC in INR signaling, and for identifying subjects having a predisposition to
 CC such diseases associated with INR signaling. The present sequence is an
 CC ISM protein described in the exemplification of the invention.

XX Sequence 298 AA;

Query Match 99.4%; Score 1537; DB 23; Length 298;
 Best Local Similarity 99.3%; Pred. No. 2.6e-153;
 Matches 296; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTDAALSPAKDPLAGGVAALSKTAVAPIERVKLLQVQHSKQITADKQYGIIDCVVR 60
 DB 1 MTDAALSPAKDPLAGGVAALSKTAVAPIERVKLLQVQHSKQITADKQYGIIDCVVR 60
 QY 61 IPKQEVLSFWRGNLANVIRFFPTQALNFAFKDKTKQIFLGVDKRTQFWRYFAGNLASG 120
 DB 61 IPKQGVLSFWRGNLANVIRFFPTQALNFAFKDKTKQIFLGVDKRTQFWRYFAGNLASG 120
 QY 121 GAAGATSLCFYVPLDPARTRLADVGKAGABERFRLGDDCLVKIYKSDGIRGLYOGFVS 180
 DB 121 GAAGATSLCFYVPLDPARTRLADVGKAGABERFRLGDDCLVKIYKSDGIRGLYOGFVS 180
 QY 181 VQGIITRYAAAFGYIDTAKGMLPDPKNTHTIVSMNIAQTVAVAGLTSYPPDYRRRRMM 240
 DB 181 VQGIITRYAAAFGYIDTAKGMLPDPKNTHTIVSMNIAQTVAVAGLTSYPPDYRRRRMM 240
 QY 241 QSGRKGTDIMVTGTLDCWRKIARDGKAFPKGAMSVNLRGAGFVLYVDEIKKYT 298
 DB 241 QSGRKGTDIMVTGTLDCWRKIARDGKAFPKGAMSVNLRGAGFVLYVDEIKKYT 298

RESULT 5

ID AAY71033 standard; Protein; 298 AA.

AC AAY71033;

DT 29-AUG-2000 (first entry)

DE Human adenine nucleotide translocator ANT3.

XX Human, adenine nucleotide translocator; ANT3; mitochondria; ADP, ATP;
 KW adenosine triphosphate; adenosine triphosphate; apoptosis; MPT; cancer;
 KW mitochondrial permeability transition; neuroprotective; neurotrophic;
 KW antiParkinsonian; cytoskeletal; antidiabetic; anticonvulsant; neuroleptic;
 KW antiapoptotic; cerebroprotective; therapeutic; secretory; peptidase;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
 KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
 KW mitochondrial diabetes and deafness; hyperproliferative disorder;
 KW myoclonic epilepsy red ragged fibre syndrome.

XX Homo sapiens.

OS WO200026370-A2.

PN 11-MAY-2000.

PD 03-NOV-1999; 99WO-US25883.

PR 03-NOV-1998; 98US-0185904.

PR 08-SEP-1999; 99US-0393441.

XX (MITO-) MITOKOR.

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR,
 PI Ghosh SS;

XX MPI; 2000-365619/31.

XX N-PSDB; AAD00521.

XX Recombinant construct encoding adenine nucleotide translocator

PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -

XX Claim 46; Page 173-174; 175pp; English.

CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression of
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, peptidase, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MTDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT3 from human brain.

XX Sequence 298 AA;

Query Match 94.0%; Score 1454; DB 21; Length 298;
 Best Local Similarity 92.6%; Pred. No. 1.4e-144;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTDAALSPAKDPLAGGVAALSKTAVAPIERVKLLQVQHSKQITADKQYGIIDCVVR 60
 DB 1 MTDAALSPAKDPLAGGVAALSKTAVAPIERVKLLQVQHSKQITADKQYGIIDCVVR 60
 QY 61 IPKQEVLSFWRGNLANVIRFFPTQALNFAFKDKTKQIFLGVDKRTQFWRYFAGNLASG 120
 DB 61 IPKQGVLSFWRGNLANVIRFFPTQALNFAFKDKTKQIFLGVDKRTQFWRYFAGNLASG 120
 QY 121 GAAGATSLCFYVPLDPARTRLADVGKAGABERFRLGDDCLVKIYKSDGIRGLYOGFVS 180
 DB 121 GAAGATSLCFYVPLDPARTRLADVGKAGABERFRLGDDCLVKIYKSDGIRGLYOGFVS 180
 QY 181 VQGIITRYAAAFGYIDTAKGMLPDPKNTHTIVSMNIAQTVAVAGLTSYPPDYRRRRMM 240
 DB 181 VQGIITRYAAAFGYIDTAKGMLPDPKNTHTIVSMNIAQTVAVAGLTSYPPDYRRRRMM 240
 QY 241 QSGRKGTDIMVTGTLDCWRKIARDGKAFPKGAMSVNLRGAGFVLYVDEIKKYT 296
 DB 241 QSGRKGTDIMVTGTLDCWRKIARDGKAFPKGAMSVNLRGAGFVLYVDEIKKYT 296

RESULT 6

ID AAM39641 standard; Protein; 298 AA.

AC AAM39641;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 2786.

XX Human, neurotrophic; immunosuppressant; cytoskeletal; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.

XX Homo sapiens.

OS WO200153312-A1.

PN 26-JUL-2001.

Qy	181	VOGIIITVAAAYAGVIDTAKGMLEDPENKNTIVISMMIAQVTVVAGLTSVPEPTVRBRMM	24
Db	181	VOGIIITVAAAYAGVIDTAKGMLEDPENKNTIVISMMIAQVTVVAGLTSVPEPTVRBRMM	240
Qy	241	QSGRGKTDIMYTGTLDCWRKRIARDEGKAFFPKGAMSNVLRGKGAFVLVYDEIKK	296
Db	241	QSGRGKADIMYTGTVDCWRKRIFRDEGKGAFPKGAMSNVLRGKGAFVLVYDELKK	296
RESULT 8			
ID	AAU10380	standard; Protein; 298 AA.	
XX	AAU10380;		
AC	14-FEB-2002	(first entry)	
XX			
DE	Human adenine nucleotide translocator 3 (ANT3).		
DE	Human; adenine nucleotide translocator; ANT;		
KW	mitochondrial matrix protein.		
OS	Homo sapiens.		
XX	MO200185944-A2.		
XX	15-NOV-2001.		
XX	11-MAY-2001; 2001MO-US15416.		
XX	11-MAY-2000; 2000US-0569327.		
XX	(MITO-) MITOKOR.		
PA	Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;		
PI	Ghosh SS, Moos WH, Pel Y, Carroll AK;		
XX	MP1; 2002-055598/07.		
DR	N-PSDB; AAS16690.		
XX			
PT	Novel recombinant expression construct for producing adenine nucleotide		
PT	translocator polypeptides, comprises a regulated promoter linked to		
PT	nucleic acid encoding the polypeptide		
XX			
PS	Example 3; Fig 2; 147pp; English.		
XX			
CC	The invention relates to a recombinant expression construct (I)		
CC	comprising a regulated promoter operably linked to a nucleic acid		
CC	encoding an adenine nucleotide translocator (ANT) polypeptide. ANT		
CC	proteins mediate the exchange of ATP synthesised in the mitochondrial		
CC	matrix for ADP in the cytosol. (I) is useful for producing recombinant		
CC	ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and		
CC	culturing the host cell. (I) is also useful for targeting a polypeptide		
CC	of interest to a mitochondrial membrane, where ANT polypeptide is		
CC	expressed as a fusion protein with the polypeptide of interest.		
CC	Recombinant ANT polypeptide, or cells expressing the polypeptide, is		
CC	useful for identifying an agent that binds to an ANT polypeptide. ANT		
CC	ligand is useful for determining the presence of an ANT polypeptide;		
CC	preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating		
CC	ANT from a biological sample, where the ANT ligand is covalently or non-		
CC	covalently bound to a solid phase. Detectably labeled ANT ligand is also		
CC	useful for identifying an agent that interacts with an ANT polypeptide.		
CC	The present sequence represents the amino acid sequence of human ANT3.		
XX			
XX	Sequence 298 AA;		
XX			
Query Match	94.0%; Score 1454; DB 23; Length 298;		
Best Local Similarity	92.6%; Pred. No. 1.4e-144;		
Matches 274;	Conservative 13; Mismatches 9; Indels 0; Gaps 0		
Qy	1	WTDAALSAFKDPLAGGVAANAISKTVAPIERVKLLIQVHASKQITADKQYGIIDCVVR	60

Db	1	MTGQASISAKPOFLAGGIAAASISKTAVAPIERKLLQVHASQKQIADQKQKGIIVDCIYR	60
Qy	61	IPKEQEVISPMRGNLANVIRIFPTQALNFAFDOKTKQIITLGGYDKRTQEMRYFAGNLASG	120
Db	61	IPKEQGVISPMRGNLANVIRIFPTQALNFAFDOKTKQIITLGGYDKRTQEMRYFAGNLASG	120
Qy	121	GAAGTSTLCFVYPLFAPTRFLAADYQKGAEREPRGLGDCLVKIKYSDGIKGLYQGFNVIS	180
Db	121	GAAGTSTLCFVYPLFAPTRFLAADYQKGSSTEREPRGLGDCLVKIKYSDGIRGLYQGFNVIS	180
Qy	181	VOGIIITVFAAYEGIVDTAKGMLPDPKNTHTIVISWMLAQTVTAVAGLTSYPPDTRRRMM	240
Db	181	VOGIIITVFAAYEGIVDTAKGMLPDPKNTHTIVISWMLAQTVTAVAGVSYPPDTRRRMM	240
Qy	241	QSGRRKTDIMYTTGLDCKWRKIARDEGKKAFFFGAGNSNVLRGGAAYVLYLYDEIKK	296
Db	241	QSGRRKADIMYTGIVDCWRKIIFRDEGKKAFFFGAGNSNVLRGGAFVLYLYDELKK	296
RESULT 9			
ID	AA041427	standard; Protein; 323 AA.	
XX	AA041427;		
XX	AA041427;		
DT	22-OCT-2001	(first entry)	
DE	Human polypeptide SEQ ID NO 6358.		
XX			
KW	Human, nootropic; immunosuppressant; cyostatic; gene therapy; cancer;		
KW	peripheral nervous system; neuropathy; central nervous system; CNS;		
KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;		
KW	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;		
KW	chemokine; thrombolytic; drug screening; arthritis; inflammation;		
KW	leukemia.		
OS	Homo sapiens.		
XX			
PN	WO200153312-A1.		
XX			
PD	26-JUL-2001.		
XX			
PF	26-DEC-2000; 2000WO-US34263.		
XX			
PR	21-JAN-2000; 2000US-0488725.		
PR	25-APR-2000; 2000US-0552317.		
PR	09-JUL-2000; 2000US-0598042.		
PR	19-JUL-2000; 2000US-0620312.		
PR	03-AUG-2000; 2000US-0653450.		
PR	14-SEP-2000; 2000US-0662191.		
PR	19-OCT-2000; 2000US-0693036.		
PR	29-NOV-2000; 2000US-0727344.		
XX			
PA	(HYSB-) HYSB INC.		
XX			
PI	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;		
PI	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;		
PI	Zhao QH, Zhou P, Goodrich R, Drmanac RT;		
XX			
DR	WPI, 2001-442253/47.		
XX			
XX	N-PSDB; AAI60583.		
PT			
XX	Novel nucleic acids and polypeptides, useful for treating disorders		
PT	such as central nervous system injuries -		
XX			
PS	Example 2; SEQ ID NO 6358; 10078bp; English.		
XX			
CC	The invention relates to human nucleic acids (AAI57798-AAI61369) and		
CC	the encoded polypeptides (AAI8642-AAI42213) with nootropic,		
CC	immunosuppressant and cytostatic activity. The polynucleotides are useful		
CC	in gene therapy. A composition containing a polypeptide or polynucleotide		
CC	of the invention may be used to treat diseases of the peripheral nervous		
CC	system, such as peripheral nervous injuries, peripheral neuropathy and		

XX WO9819714-A1.
 XX 14-MAY-1998.
 XX
 XX 31-OCT-1997; 97WO-US19882.
 XX
 XX 01-NOV-1996; 96US-0030017.
 XX
 XX (UYEM-) UNIV EMORY.
 XX
 XX Graham BC, Macgregor GR, Wallace DC;
 XX WPI; 1998-286608/25.
 XX N-PSDB; AAV36479.
 XX
 XX Mice lacking heart-muscle adenine nucleotide translocator protein -
 PT useful as model for mitochondrial myopathy and hypertrophic
 PT cardiomyopathy in animals and to test therapeutic compositions or
 PT gene therapies
 XX
 XX PS Disclosure; Page 39-40; 61pp; English.
 XX
 CC The present sequence is the mouse Anti protein, the cDNA producing this
 CC polypeptide is cloned by screening a mouse heart cDNA library with the
 CC human Anti cDNA as a probe. The Anti cDNA sequence was determined by DNA
 CC Tag deoxy terminator cycle sequencing. The Anti protein is encoded by
 CC the Anti locus, a nuclear gene on chromosome 8. This protein is required
 CC in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP
 CC which can then be converted into ATP. An Anti homozygous mutant would
 CC thus be defective in OXPHOS which results in disease in oxidative
 CC metabolism dependent tissues. This mouse Anti homozygous mutant can be
 CC used as a model system for fascioscapular humeral muscular dystrophy,
 CC hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model
 CC systems can be used to test possible therapeutic compounds which
 CC increase/mediate ATP and ADP exchange across the mitochondrial membrane
 CC independent of ANT1.
 CC
 XX
 XX SQ Sequence 298 AA;

Query Match 91.2%; Score 1411; DB 19; Length 298;
 Best Local Similarity 89.2%; Pred. No. 4.9e-140;
 Matches 265; Conservative 15; Mismatches 17; Indels 0; Gaps 0;
 QY 1 MTDALSPAKDFLAGVAAISKTAVAPIERVKLLQVOHASKQITADKQYGIIDCVVR 60
 DB 1 MGDQALSLFKDFLAGVAAVSKTAVAPIERVKLLQVOHASKQISAEKQYGIIDCVVR 60
 QY 61 IPKEQEVLSFMRGNLANVIRYPTQALNFAFKDKTKQIFLGVDKRTQFMRYPAGNLASG 120
 DB 61 IPKEGFLSPMRGNLANVIRYPTQALNFAFKDKTKQIFLGVDKRTQFMRYPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLAADVGKAGAREFRGLDCLVKIYKSDGIKGLYOGFNVSV 180
 DB 121 GAAGATSLCFVYPLDFARTRLAADVGKAGAREFRGLDCLVKIYKSDGIKGLYOGFNVSV 180
 QY 181 VOGIIYYRAAYFGIYDTAKGMLPDPKXNTHIIVSMIAQCTTAVAGLTSYPTVRRMM 240
 DB 181 VOGIIYYRAAYFGIYDTAKGMLPDPKXNTHIIVSMIAQCTTAVAGLTSYPTVRRMM 240
 QY 241 QSGRGKTDIMTGTLDCKRKIARDGKGAFFKAGANSVLKMGCAFVLVLDKIKKY 297
 DB 241 QSGRGKADIMYTGTLDCWRKIADKDEGANAFKAGANSVLKMGCAFVLVLDKIKKY 297

RESULT 12

ABUS3219
 ID ABUS3219 standard; Protein; 293 AA.
 XX
 XX AC ABUS3219;
 XX
 XX DT 14-APR-2003 (first entry)
 XX

DE Human metabolism-associated DKFZp35n12 homologue #1.
 XX Human; gene therapy; vaccine; disease treatment; detection.
 XX Homo sapiens.
 XX WO200112659-A2.
 XX
 XX 22-FEB-2001.
 XX
 XX 18-AUG-2000; 2000WO-IB01496.
 XX
 XX 18-AUG-1999; 99US-0149499.
 XX 28-SEP-1999; 99US-0156503.
 XX
 XX (GERU-) GERMAN HUMAN GENOME PROJECT.
 XX
 XX Wiemann S;
 XX WPI; 2001-327840/34.
 XX
 XX Nucleic acids having the sequences of clones isolated from libraries of
 PT different human tissues, useful in recombinant DNA methodologies -
 PT
 XX
 XX PS Example III; Page 850; 1095pp; English.
 XX
 CC This invention describes novel polynucleotides and polypeptides isolated
 CC from human cDNA libraries which can be used for gene therapy or in
 CC vaccines. The polynucleotides of the invention and antibodies encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate polypeptide expression. The products of the
 CC invention may also be used to identify modulators of expression and
 CC activity and to down regulate expression and activity. The antibodies of
 CC the invention may also be used as diagnostic agents for detecting the
 CC presence of polypeptides in samples. This sequence represents a homologue
 CC of a polypeptide described in the disclosure of the invention.
 CC
 XX
 XX SQ Sequence 293 AA;

Query Match 91.1%; Score 1409; DB 22; Length 293;
 Best Local Similarity 90.1%; Pred. No. 7.7e-140;
 Matches 264; Conservative 15; Mismatches 14; Indels 0; Gaps 0;
 QY 5 ALSPAKDFLAGVAAISKTAVAPIERVKLLQVOHASKQITADKQYGIIDCVVRIPKE 64
 DB 1 ALSPKDFLAGVAAVSKTAVAPIERVKLLQVOHASKQISAEKQYGIIDCVVRIPKE 60
 QY 65 QEVLSFMRGNLANVIRYPTQALNFAFKDKTKQIFLGVDKRTQFMRYPAGNLASGAG 124
 DB 61 QGFLSPMRGNLANVIRYPTQALNFAFKDKTKQIFLGVDKRTQFMRYPAGNLASGAG 120
 QY 125 ATSLCFVYPLDFARTRLAADVGKAGAREFRGLDCLVKIYKSDGIKGLYOGFNVSV 184
 DB 121 ATSLCFVYPLDFARTRLAADVGKAGAREFRGLDCLVKIYKSDGIKGLYOGFNVSV 180
 QY 185 IYRAAYFGIYDTAKGMLPDPKXNTHIIVSMIAQCTTAVAGLTSYPTVRRMM 244
 DB 181 IYRAAYFGIYDTAKGMLPDPKXNTHIIVSMIAQCTTAVAGLTSYPTVRRMM 240
 QY 245 KGTIDIMTGTLDCKRKIARDGKGAFFKAGANSVLKMGCAFVLVLDKIKKY 297
 DB 241 KGADIMYTGTLDCWRKIADKDEGANAFKAGANSVLKMGCAFVLVLDKIKKY 293

RESULT 13

AA71031
 ID AA71031 standard; Protein; 297 AA.
 XX
 XX AC AA71031;
 XX
 XX DT 29-AUG-2000 (first entry)
 XX
 XX Human adenine nucleotide translocator ANT1.

XX Human; adenine nucleotide translocator; ANT1; mitochondria; ADP; ATP;
 KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
 KW mitochondrial permeability transition; neuroprotective; neurologic;
 KW antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
 KW antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
 KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
 KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
 KW mitochondrial diabetes and deafness; hyperproliferative disorder;
 KW myoclonic epilepsy red ragged fibre syndrome.
 XX Homo sapiens.
 OS WO200026370-A2.
 XX PD 11-MAY-2000.
 XX PF 03-NOV-1999; 99WO-US25883.
 XX PR 03-NOV-1998; 98US-0185904.
 XX PR 08-SEP-1999; 99US-0393441.
 XX PA (MITO-) MITOKOR.
 XX PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;
 XX PI Ghosh S;
 XX DR WPI; 2000-365619/31.
 XX DR N-PSDB; AAD00519.
 XX PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 XX PS Claim 44; Page 172; 175pp; English.
 XX CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression of
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT1 from human brain.
 XX SQ Sequence 297 AA;
 XX Query Match 89.9%; Score 1391.5; DB 21; Length 297;
 XX Best Local Similarity 88.6%; Pred. No. 5.5e-138;
 XX Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;
 QY 1 MTDAALSPAKDPLAGGVAALASTKAVAPRIERVKLLQVQHSKQITADKQKGIIDCVR 60
 Db 1 MGDHAWSLKDFLGAVALAAVSKTAVAPRIERVKLLQVQHSKQISAKQYKGIIDCVR 60
 QY 61 IPKQEVLSFMRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFMVYFAGNTASG 120
 Db 61 IPKQGFISFMRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFMVYFAGNTASG 120
 QY 121 GAAGTSLCFYVPIIDFARTLADVGKAGAEERFGDGLVKIKYSDGINKLYGQFNVS 180
 Db 121 GAAGTSLCFYVPIIDFARTLADVGRR-AQREFFHGLDCCIKIKFSGDLGKLYGQFNVS 179

QY 181 VQGIITRAAYFGIYDTAKGMLPDPKNTHTIVISWMIQOTYAVAGLTSYEDTVRRMM 240
 Db 180 VQGIITRAAYFGIYDTAKGMLPDPKNTHTIVISWMIQOTYAVAGLTSYEDTVRRMM 239
 QY 241 QSGRKGTDIMVYTGTLDCWRKIARDDEGKAPFKGAMSVNLKMGAPVLVYDEIKKY 297
 Db 240 QSGRKGADIMVYTGTCWRKIARDDEGKAPFKGAMSVNLKMGAPVLVYDEIKKY 296
 RESULT 14
 AAU01198
 ID AAU01198 standard; Protein; 297 AA.
 XX AC AAU01198;
 XX DT 07-SEP-2001 (first entry)
 XX DE Human adenine nucleotide translocator-1 (ANT-1) protein.
 XX KW Human; adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX Homo sapiens.
 OS WO200132876-A2.
 XX PD 10-MAY-2001.
 XX PF 03-NOV-2000; 2000WO-US30535.
 XX PR 03-NOV-1999; 99US-0434354.
 XX PA (MITO-) MITOKOR.
 XX PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
 XX PI Velezlebi G, Davis RE;
 XX DR WPI; 2001-291054/30.
 XX DR N-PSDB; AAS05901.
 XX PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX PS Disclosure; Fig 2; 186pp; English.
 XX CC The present sequence represents human adenine nucleotide translocator-1
 CC (ANT-1) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 XX SQ Sequence 297 AA;
 XX Query Match 89.9%; Score 1391.5; DB 22; Length 297;
 XX Best Local Similarity 88.6%; Pred. No. 5.5e-138;

Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTDALSPAKDFLAGVAAAIKTAAPARIVKLLQVQHASKOITADKQYKGIIDCVYR 60
 DB 1 MGDHMSFLKDFLAGVAAAVKTAAPARIVKLLQVQHASKOITADKQYKGIIDCVYR 60

QY 61 IPKEGEVLSFWRGNLANVIRYPTQALNFAFDKXKQIFLGVDKRTQPMRYFAGNLASG 120
 DB 61 IPKEGEVLSFWRGNLANVIRYPTQALNFAFDKXKQIFLGVDKRTQPMRYFAGNLASG 120

QY 121 GAAGATSLCFYYPPLDFAFTRLAADVGR-AQREFHGLDCLIKIKSDGLRGLYQGFNVS 180
 DB 121 GAAGATSLCFYYPPLDFAFTRLAADVGR-AQREFHGLDCLIKIKSDGLRGLYQGFNVS 180

QY 181 VGGIITVRAAYFGIYDPAKGMPLDPKXTHIVISWMLAQVTVAAGLTSYPTVRRMM 240
 DB 180 VGGIITVRAAYFGIYDPAKGMPLDPKXTHIVISWMLAQVTVAAGLTSYPTVRRMM 240

QY 241 QSGRKGTDIMYTGTLDCWRKILARDEGKAFKFGAMSNVLRGMGAFVLYLDEIKKY 297
 DB 240 QSGRKGADIMYTGTLDCWRKILARDEGKAFKFGAMSNVLRGMGAFVLYLDEIKKY 296

RESULT 15

AAU10378 standard; Protein; 297 AA.

AAU10378;

14-FEB-2002 (first entry)

Human adenine nucleotide translocator 1 (ANT1).

Human; adenine nucleotide translocator; ANT;

mitochondrial matrix protein.

Homo sapiens.

W0200185944-A2.

15-NOV-2001.

11-MAY-2001; 2001WO-US15416.

11-MAY-2000; 2000US-0569327.

(MITO-) MITOKOR.

Andersen CM, Davis RE, Cleverger W, Wiley SE, Miller SW, Szabo TR;

Ghosh SS, Moos WH, Pel Y, Carroll AK;

MPI; 2002-055598/07.

N-PSDB; AAS16688.

Claim 44; Fig 2; 147pp; English.

The invention relates to a recombinant expression construct (I) comprising a regulated promoter operably linked to a nucleic acid encoding an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesised in the mitochondrial matrix for ADP in the cytosol. (I) is useful for producing recombinant ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and culturing the host cell. (I) is also useful for targeting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is expressed as a fusion protein with the polypeptide of interest.

Recombinant ANT polypeptide, or cells expressing the polypeptide, is useful for identifying an agent that binds to an ANT polypeptide. ANT ligand is useful for determining the presence of an ANT polypeptide, preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating

CC ANT from a biological sample, where the ANT ligand is covalently or non-covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. The present sequence represents the amino acid sequence of human ANT1.

SQ Sequence 297 AA;

Query Match 89.9%; Score 1391.5; DB 23; Length 297;

Best Local Similarity 88.6%; Pred. No. 5.5e-138;

Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTDALSPAKDFLAGVAAAIKTAAPARIVKLLQVQHASKOITADKQYKGIIDCVYR 60
 DB 1 MGDHMSFLKDFLAGVAAAVKTAAPARIVKLLQVQHASKOITADKQYKGIIDCVYR 60

QY 61 IPKEGEVLSFWRGNLANVIRYPTQALNFAFDKXKQIFLGVDKRTQPMRYFAGNLASG 120
 DB 61 IPKEGEVLSFWRGNLANVIRYPTQALNFAFDKXKQIFLGVDKRTQPMRYFAGNLASG 120

QY 121 GAAGATSLCFYYPPLDFAFTRLAADVGR-AQREFHGLDCLIKIKSDGLRGLYQGFNVS 180
 DB 121 GAAGATSLCFYYPPLDFAFTRLAADVGR-AQREFHGLDCLIKIKSDGLRGLYQGFNVS 179

QY 181 VGGIITVRAAYFGIYDPAKGMPLDPKXTHIVISWMLAQVTVAAGLTSYPTVRRMM 240
 DB 180 VGGIITVRAAYFGIYDPAKGMPLDPKXTHIVISWMLAQVTVAAGLTSYPTVRRMM 239

QY 241 QSGRKGTDIMYTGTLDCWRKILARDEGKAFKFGAMSNVLRGMGAFVLYLDEIKKY 297
 DB 240 QSGRKGADIMYTGTLDCWRKILARDEGKAFKFGAMSNVLRGMGAFVLYLDEIKKY 296

Search completed: December 18, 2003, 12:40:46

Job time : 35.3729 secs

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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:38:52 ; Search time 12.3471 Seconds
(without alignments)
1021.178 Million cell updates/sec

Title: US-09-811-131-32

Perfect score: 1547
Sequence: 1 MTDAALSPAKOFLAGVAA.....LRGMGAFLVLYDEIKKYT 298

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310658 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgm2_6/ptodata/1/1aa/5A.COMB.pep: *
2: /cgm2_6/ptodata/1/1aa/5B.COMB.pep: *
3: /cgm2_6/ptodata/1/1aa/6A.COMB.pep: *
4: /cgm2_6/ptodata/1/1aa/6B.COMB.pep: *
5: /cgm2_6/ptodata/1/1aa/PTCUTS.COMB.pep: *
6: /cgm2_6/ptodata/1/1aa/backfilest.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1547	100.0	298	4	US-09-434-354-48
2	1454	94.0	298	4	US-09-434-354-49
3	1411	91.2	298	3	US-08-961-871-10
4	1391.5	89.9	297	4	US-09-434-354-47
5	302	19.5	469	4	US-09-996-243-289
6	301	19.5	469	3	US-09-188-930-339
7	301	19.5	469	4	US-09-312-283C-339
8	274	17.7	291	4	US-09-501-558-2
9	274	17.7	335	4	US-09-482-273-118
10	261.5	16.9	447	4	US-09-160-119-4
11	261.5	16.9	447	4	US-09-160-119-2
12	247	16.0	312	3	US-09-142-565-2
13	244.5	15.8	311	2	US-08-775-009-33
14	239.5	15.5	309	1	US-08-518-878B-51
15	239.5	15.5	309	2	US-08-807-861A-51
16	238.5	15.5	309	2	US-08-470-868A-51
17	238.5	15.5	309	3	US-09-210-681-51
18	239.5	15.5	309	3	US-08-946-719A-51
19	239.5	15.5	309	4	US-09-547-983-51
20	236.5	15.3	299	1	US-08-518-878B-56
21	236.5	15.3	299	2	US-08-470-868A-56
22	232.5	15.0	311	2	US-08-775-009-32
23	230.5	14.9	320	2	US-08-933-750C-12
24	230.5	14.9	320	3	US-09-234-613-12
25	227	14.7	308	2	US-08-937-466-2
26	227	14.7	308	2	US-09-172-528-2
27	227	14.7	308	3	US-09-318-199-2

28	227	14.7	308	3	US-09-503-579-2	Sequence 2, Appl1
29	223	14.4	432	2	US-08-937-466-4	Sequence 4, Appl1
30	223	14.4	432	2	US-08-172-528-4	Sequence 4, Appl1
31	223	14.4	432	3	US-09-318-159-4	Sequence 4, Appl1
32	219.5	14.2	432	3	US-09-503-579-4	Sequence 4, Appl1
33	218.5	14.1	303	1	US-08-294-522B-36	Sequence 36, Appl1
34	217.5	14.1	303	1	US-08-518-878B-37	Sequence 37, Appl1
35	217.5	14.1	303	2	US-08-807-861A-37	Sequence 37, Appl1
36	217.5	14.1	303	2	US-08-470-868A-37	Sequence 37, Appl1
37	217.5	14.1	303	3	US-09-210-681-37	Sequence 37, Appl1
38	217.5	14.1	303	3	US-08-946-719A-37	Sequence 37, Appl1
39	217.5	14.1	303	4	US-09-547-983-37	Sequence 37, Appl1
40	217.5	14.1	328	3	US-09-068-140A-15	Sequence 15, Appl1
41	191	12.3	256	2	US-08-937-466-6	Sequence 6, Appl1
42	190.5	12.3	256	2	US-09-172-528-6	Sequence 6, Appl1
43	190.5	12.3	256	3	US-09-318-159-6	Sequence 6, Appl1
44	190.5	12.3	256	3	US-09-503-579-6	Sequence 6, Appl1
45	190.5	12.3	256	3	US-09-503-579-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-09-434-354-48

Sequence 48, Application US/09434354
Patent No. 6562563

GENERAL INFORMATION:

APPLICANT: Murphy, Anne N.

APPLICANT: Clevenger, William

APPLICANT: Wiley, Sandra Eileen

APPLICANT: Andreyev, Alexander Y.

APPLICANT: Frigeri, Luciano G.

APPLICANT: Velicelebi, Gonul

APPLICANT: Davis, Robert E.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING

TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR

TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS

FILE REFERENCE: 660086.433

CURRENT FILING DATE: 1999-11-03

CURRENT OF SEQ ID NOS: 54

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 48

LENGTH: 298

TYPE: PRT

ORGANISM: Homo sapien

US-09-434-354-48

Query Match 100.0%; Score 1547; DB 4; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.2e-169;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTDAALSPAKOFLAGVAAATSKTAVAPTEEVKLLLOVQHASKOITADKOYKGIIDCVR	60
DB	1	MTDAALSPAKOFLAGVAAATSKTAVAPTEEVKLLLOVQHASKOITADKOYKGIIDCVR	60
QY	61	IPKQEVLSFMRGNLANVIRYPTQALNFAKDKYKQIFLGVNKRTPMRYFPAAGTASG	120
DB	61	IPKQEVLSFMRGNLANVIRYPTQALNFAKDKYKQIFLGVNKRTPMRYFPAAGTASG	120
QY	121	GAAGTSLCFYTPIDFATRLAADVGRAGARERRGIDCLVYKSGIGLYQGFVNS	180
DB	121	GAAGTSLCFYTPIDFATRLAADVGRAGARERRGIDCLVYKSGIGLYQGFVNS	180
QY	181	VQGIIRAAVFGYIDRAKGLPDKNTHIVISMIAQTVAVAGLSYPPDTRRRMM	240
DB	181	VQGIIRAAVFGYIDRAKGLPDKNTHIVISMIAQTVAVAGLSYPPDTRRRMM	240
QY	241	QSGRGTIDIMVTGTLDCWRKIARDEGKAPFGKAMSVNLRMGAFVLYVDEIKKYT	298
DB	241	QSGRGTIDIMVTGTLDCWRKIARDEGKAPFGKAMSVNLRMGAFVLYVDEIKKYT	298

RESULT 2
US-09-434-354-49
Sequence 49, Application US/09434354
Patent No. 6562563
GENERAL INFORMATION:
APPLICANT: Murphy, Anne N.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Bileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Frigieri, Luciano G.
APPLICANT: Velicelcbl, Gonul
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
FILE REFERENCE: 660088.433
CURRENT FILING DATE: 1999-11-03
CURRENT APPLICATION NUMBER: US/09/434,354
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 49
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-434-354-49

Query Match 94.0%; Score 1454; DB 4; Length 298;
Best Local Similarity 92.6%; Pred. No. 6.3e-159;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKOITADKOYKGIIDCVR 60
DB 1 MTEQGISAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKOITADKOYKGIIDCVR 60
QY 61 IPKEQEVLSFPRKGNLANVIRYPTQALNFAFKDKYKQIFLGVDVGRQTFMRYFAGNLASG 120
DB 61 IPKEQGVLSFPRKGNLANVIRYPTQALNFAFKDKYKQIFLGVDVGRQTFMRYFAGNLASG 120
QY 121 GAAAGTSLCFYYPDPARTRLAADVKGAGAREFRGLDCLVKIYKSGIGLQYGFVS 180
DB 121 GAAAGTSLCFYYPDPARTRLAADVKGAGAREFRGLDCLVKIYKSGIGLQYGFVS 180
QY 181 VGGIITRAAYFGYVDTAKGMLPDPKNTHTIVISWIAQTVTAAGLTSYPPDVTARRMM 240
DB 181 VGGIITRAAYFGYVDTAKGMLPDPKNTHTIVISWIAQTVTAAGLTSYPPDVTARRMM 240
QY 241 QSGRKGADIMVTGTLDCWRKIARDGKAFPKGAMSNVLRGMGAFVLVYDEIKY 296
DB 241 QSGRKGADIMVTGTLDCWRKIARDGKAFPKGAMSNVLRGMGAFVLVYDEIKY 296

RESULT 3

US-08-961-871-10
Sequence 10, Application US/08961871
Patent No. 6013858
GENERAL INFORMATION:
APPLICANT: Wallace, Douglas C.
APPLICANT: Graham, Brett H.
APPLICANT: Macgregor, Grant R.
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Reiber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-08-961-871-10

Query Match 91.2%; Score 1411; DB 3; Length 298;
Best Local Similarity 89.2%; Pred. No. 5.6e-154;
Matches 265; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKOITADKOYKGIIDCVR 60
DB 1 MGDOLSLKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKOITADKOYKGIIDCVR 60
QY 61 IPKEQEVLSFPRKGNLANVIRYPTQALNFAFKDKYKQIFLGVDVGRQTFMRYFAGNLASG 120
DB 61 IPKEQGVLSFPRKGNLANVIRYPTQALNFAFKDKYKQIFLGVDVGRQTFMRYFAGNLASG 120
QY 121 GAAAGTSLCFYYPDPARTRLAADVKGAGAREFRGLDCLVKIYKSGIGLQYGFVS 180
DB 121 GAAAGTSLCFYYPDPARTRLAADVKGAGAREFRGLDCLVKIYKSGIGLQYGFVS 180
QY 181 VGGIITRAAYFGYVDTAKGMLPDPKNTHTIVISWIAQTVTAAGLTSYPPDVTARRMM 240
DB 181 VGGIITRAAYFGYVDTAKGMLPDPKNTHTIVISWIAQTVTAAGLTSYPPDVTARRMM 240
QY 241 QSGRKGADIMVTGTLDCWRKIARDGKAFPKGAMSNVLRGMGAFVLVYDEIKY 297
DB 241 QSGRKGADIMVTGTLDCWRKIARDGKAFPKGAMSNVLRGMGAFVLVYDEIKY 297

RESULT 4

US-09-434-354-47
Sequence 47, Application US/09434354
Patent No. 6562563
GENERAL INFORMATION:
APPLICANT: Murphy, Anne N.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Bileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Frigieri, Luciano G.
APPLICANT: Velicelcbl, Gonul
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
FILE REFERENCE: 660088.433
CURRENT FILING DATE: 1999-11-03
CURRENT APPLICATION NUMBER: US/09/434,354
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 47
LENGTH: 297
TYPE: PRT
ORGANISM: Homo sapien

US-09-434-354-47

Query Match 89.9%; Score 1391.5; DB 4; Length 297;
 Best Local Similarity 88.6%; Pred. No. 9.8e-152;
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTDAALSPAKDFLAGVAAAIKSTAVADIERVKLLQVQHASKQITADKQYGIIDCVVR 60
 DB 1 MGDHMSFLKDFLNGAVAAVSKTAVADIERVKLLQVQHASKQISAKQYGIIDCVVR 60
 QY 61 IPKGEVLSFMRGNLANIRYPTQALNPAFKDKTKQIFLGGVDKRTQFMRYPAGNLASG 120
 DB 61 IPKGEVLSFMRGNLANIRYPTQALNPAFKDKTKQIFLGGVDKRTQFMRYPAGNLASG 120
 QY 121 GAAGATSLCFYPPDLPARTLADVKGAGAREPFGLDLCVKKYKSGDGLVQGFVNS 180
 DB 121 GAAGATSLCFYPPDLPARTLADVKGAGAREPFGLDLCVKKYKSGDGLVQGFVNS 179
 QY 181 VQGIIVRAAYFGYVDIAKGMLPDPKNTHTVLSNMIAQVTAVAGLTSYPPDVRRRMM 240
 DB 180 VQGIIVRAAYFGYVDIAKGMLPDPKNTHTVLSNMIAQVTAVAGLTSYPPDVRRRMM 239
 QY 241 QSGRKVDIMTGTGLDCRRTKARDEGGAFPKGANSVLRGGAFTVLVYDEIKKY 297
 DB 240 QSGRKVDIMTGTGLDCRRTKARDEGGAFPKGANSVLRGGAFTVLVYDEIKKY 296

RESULT 5
 US-09-996-243-289
 Sequence 289, Application US/09996243
 Patent No. 6478825

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Bockstein, David
 APPLICANT: Deenoyers, Luc
 APPLICANT: Batcon, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerder, Hanspeter
 APPLICANT: Gottlieb, Mary B.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavlin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas P.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730P1C13
 CURRENT APPLICATION NUMBER: US/09/996,243
 PRIOR FILING DATE: 2001-11-14
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/065186
 PRIOR FILING DATE: 1997-11-12
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066770
 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/075945
 PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/087106
 PRIOR FILING DATE: 1998-05-28
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087609
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087759
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087827
 PRIOR FILING DATE: 1998-06-03
 PRIOR APPLICATION NUMBER: 60/088021
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088025
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088026
 PRIOR FILING DATE: 1998-06-04
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 PRIOR APPLICATION NUMBER: 60/088029
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088030
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088033
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088326
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088167
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088202
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088212
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088217
 PRIOR FILING DATE: 1998-06-05
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 PRIOR FILING DATE: 1998-06-10
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 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088826
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088858
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 PRIOR APPLICATION NUMBER: 60/089105
 PRIOR FILING DATE: 1998-06-12
 PRIOR APPLICATION NUMBER: 60/089440
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089512
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089514
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089532
 PRIOR FILING DATE: 1998-06-17
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 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089598

PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02

PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 19.5%; Score 302; DB 4; Length 469;
Best Local Similarity 29.1%; Pred. No. 5.4e-26;
Matches 86; Conservative 60; Mismatches 118; Indels 32; Gaps 11;

QY 10 KDLAAGVAAIAISTAVAPIERVKLLLOVQASKOITADKOYKGIIDCVV---RIPPEQ 65
DB 188 RHVAGGAGAVSRTCTAPDLRLKVMQV-HASR-----SNMGI VGGFTQMIRREGARS 241
QY 70 FWRGNLANVIRYPTQALNPAFKDKYKOIFLGVDKRTQFWRYFAGNLAGAGATSLC 129
DB 242 LMRGGINVLKIAESAIKFMAVEQIKR--LVGSDQET---LRHERLVAGSLAGAIQS 296
QY 130 FVYPLDFARTLADVGAEREREGDCLVNTKYSDDGKGLYQGFNVSVQGIITRA 189
DB 297 SIYMEVLTKTMA--LRRTG---QYSGMLDARRILAREGVAAFKGVVPPNMLGIIPYAG 351
QY 190 AYFGIYDTAKGM-----LPDPKNTIIVISWMIAGTVAVAG-LTSYPPDYVRRMM 240
DB 352 IDLAVETLKNAMLOHVAVNSADP-----VVLACGMSSTCGLASYPALVRRMQA 407
QY 241 QSGRGTDIMYGTIDCWKRIARDEGKAFKGAWSNVLKMGAFV-LVLYDEIX 295
DB 408 QASIEGAEVETMSI--FKHILRTGEGAFGLYRGLAPNFMKVI PAVSISYVYVENIK 461

RESULT 6
US-09-188-930-339
Sequence 339, Application US/09188930A
Patent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murlison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188, 930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 339
LENGTH: 469
TYPE: PRT
ORGANISM: Mouse
US-09-188-930-339

Query Match 19.5%; Score 301; DB 3; Length 469;
Best Local Similarity 28.4%; Pred. No. 7e-26;
Matches 86; Conservative 62; Mismatches 109; Indels 46; Gaps 12;
QY 10 KDLAAGVAAIAISTAVAPIERVKLLLOVQASKOITADKOYKGIIDCVV---RIPPEQ 65
DB 188 RHVAGGAGAVSRTCTAPDLRLKVMQV-HASRNNM-----CIVGFTQMIRREG 237
QY 66 EVLSFWRGNLANVIRYPTQALNPAFKDKYKOIFLGVDKRTQFWRYFAGNLAGAGAA 125
DB 238 GAKSILMRGGINVLKIAESAIKFMAVEQIKR--LVGSDQET---LRHERLVAGSLAGA 292
QY 126 TSLCFVYPLDFARTLADVGAEREREGDCLVNTKYSDDGKGLYQGFNVSVQGIIT 185

Db 293 IAOSIVMEVLTAKTMA--LRKTYG---OYSGMLDCARRILAKEGVAFAFYKGIYPMMLGII 347
OY 186 IYRAVFGIYDTAKGMLDPPKTHI-----VISMIAQVTVAVAG--LTSYPPDT 233
Db 348 PYAGIDLAVETL-----KNTWLOQYAVNSADPGVVLACGTTISCTCQLASYPAL 400
OY 234 VRRMMOSGRKGTIDIMYTGTLDCWRKIARDEGKAFPGKAMSNTLRGGAFAV--LVLYD 292
Db 401 VRTMQAQASIEGAEVYMSL--FKQILRTGAGLGRGLAPNPMKVIIPAVISYVYE 458
OY 293 EIK 295
Db 459 NLK 461

RESULT 7
US-09-312-283C-339
Sequence 339, Application US/09312283C
Patent No. 6573095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for their Use
FILE REFERENCE: 11000.1011C2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 339
LENGTH: 469
TYPE: PRT
ORGANISM: Mouse
US-09-312-283C-339

Query Match 19.5%; Score 301; DB 4; Length 469;
Best Local Similarity 28.4%; Pred. No. 7e-26;
Matches 86; Conservative 62; Mismatches 109; Indels 46; Gaps 12;
OY 10 KDPLAGVAAAIISKAVAPIERVKLLQVHASKOITDKOYKGIIDCV---RIPKQ 65
Db 188 RHLVAGGAGAVSCTCTAPLDLKVLMQV--HASSRNN-----CIVGGFTQMIREG 237
OY 66 EVLSFWRGNLANVIRYFTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLAGGAAGA 125
Db 238 GAKSILMRNGINVLKIAPESAIKFPAVQMKR--LVGSDQET---LRTHRLVAGSLAGA 292
OY 126 TSLCFVPLDPARTRLADVGKAGAREFRGLGDCLVKIYKSDIGIKGLYOGFNVSOGII 185
Db 293 IAQSSIVMEVLTAKTMA--LRKTYG---OYSGMLDCARRILAKEGVAFAFYKGIYPMMLGII 347
OY 186 IYRAVFGIYDTAKGMLDPPKTHI-----VISMIAQVTVAVAG--LTSYPPDT 233
Db 348 PYAGIDLAVETL-----KNTWLOQYAVNSADPGVVLACGTTISCTCQLASYPAL 400
OY 234 VRRMMOSGRKGTIDIMYTGTLDCWRKIARDEGKAFPGKAMSNTLRGGAFAV--LVLYD 292
Db 401 VRTMQAQASIEGAEVYMSL--FKQILRTGAGLGRGLAPNPMKVIIPAVISYVYE 458
OY 293 EIK 295
Db 459 NLK 461

RESULT 8
US-09-501-558-2
Sequence 2, Application US/09501558
Patent No. 6403784
GENERAL INFORMATION:

APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Machowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6403784e1 Human Uncoupling Proteins and
FILE REFERENCE: Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0012-USA
CURRENT APPLICATION NUMBER: US/09/501,558
CURRENT FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 291
TYPE: PRT
ORGANISM: Homo sapiens
US-09-501-558-2

Query Match 17.7%; Score 274; DB 4; Length 291;
Best Local Similarity 27.8%; Pred. No. 4.3e-23;
Matches 85; Conservative 55; Mismatches 134; Indels 32; Gaps 9;
OY 4 AALSPADFLAGVAAAIISKAVAPIERVKLLQVHAS-----KQITADKQYKGIIDCV 58
Db 2 SALNW-KPFYVGGHASTABEGCTEPIDLTTRQLQIQGTMDAKPKKI---RYRGMHLAL 56
OY 59 VIRIKQEVLSFWRGNLANVIRYFTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLA 118
Db 57 VIRIEBGLKALVSGIAPAMLRQASGTIKIGYQSLKRLPIERPEBT-----LPINVI 111
OY 119 SGGAAGATSLCFVPLDPARTRLADVGKAGAREFRGLGDCLVKIYKSDIGIKGLYOGFN 178
Db 112 CGILSGVISTIANPTLVKIRMQASNTIOG-----GMGNFNNITQOEBTRGLMKGVS 166
OY 179 VSVQGIITIRAYAGIYDTAK-----GMLDPPKTHIIVISMIAQVTVAVAGLTSYPPD 232
Db 167 LTAQRAAIVGVSLPVVDITFKHLILSLMGDTVYTHLSF-----TCGLAGALASNPVD 222
OY 233 TVRRMMOSGRKGTIDIMYTGTLDCWRKIARDEGKAFPGKAMSNTLR--GMGAFAVLYL 290
Db 223 VRTMQAQASIEGAEVYMSL--FKQILRTGAGLGRGLAPNPMKVIIPAVISYVYE 458
OY 291 YDEIKK 296
Db 283 YEOJLK 288

RESULT 9
US-09-482-273-118
Sequence 118, Application US/09482273
Patent No. 6534531
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: P2030P1
CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,922
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,956
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 118
LENGTH: 335
TYPE: PRT
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: SITE
LOCATION: (335)

OTHER INFORMATION: Xaa equals stop translation
US-09-482-273-118

Query Match 17.7%; Score 274; DB 4; Length 335;
Best Local Similarity 28.1%; Pred. No. 5, 4e-23;
Matches 84; Conservative 51; Mismatches 134; Indels 30; Gaps 8;

QY 10 KDFLAGVAAISKTAVDPIERKLLQVQHAS-----KQITADKQYKGIIDCVRIPE 64
DB 51 KFFVVGGLASIVAEFEFTFVDLTKTLLQVQOSIDARFKFI-----KYRGMFHALFRICKE 106
QY 65 QGVLSFPMGNLANVRYEPTQALNPAFKQKQIFLGVDKRTQFRRYAGNLASGGAAG 124
DB 107 EGVLLVSGIDAPALLRQASVGTIKIGIYQSLRLEFERLEDBT-----LLIMMIGSVSG 161
QY 125 ATSLCFVYPLDPAFRLADVGKAGAREFRGLDCLVIYKSDGKGLYOGFNVSVQGI 184
DB 162 VASSTIANPTDVLKRMQO-----GSLFGSGMIGS-FIDITYOEGTRGLMRGVPTAQRA 216
QY 185 ILYRAAYFGIYDTAK-----GMLDPPKXTHIVISWMLAQVTAVAGLTSYPPDVRMM 238
DB 217 AIVGVELEPVYDITKKHLILSGMWGDTLTHFVSSF-----TCGLAGALASNPDVVRTEM 272
QY 239 MMQSGRKGDIMYTGTLDCMRKIADDEGKAFPKGAMSVNR-GMGCAFVLYLYDEIKK 296
DB 273 MMQRAIVGHVDLYKGTVDGILKMMKREGFALYKGFPMWLKLGPMNIIFFITYEQLRK 331

RESULT 10
US-09-160-119-4
Sequence 4, Application US/09160119A
Patent No. 6316219

GENERAL INFORMATION:
APPLICANT: KRIEF, STEPHANE
APPLICANT: SOUCHET, MICHEL
APPLICANT: BRIL, ANTOINE
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30985
CURRENT APPLICATION NUMBER: US/09/160,119A
CURRENT FILING DATE: 1998-09-24
EARLIER APPLICATION NUMBER: EP 97402511.6
EARLIER FILING DATE: 1997-10-23
EARLIER APPLICATION NUMBER: EP 98401655.0
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 447
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-160-119-4

Query Match 16.9%; Score 261.5; DB 4; Length 447;
Best Local Similarity 26.2%; Pred. No. 2, 3e-21;
Matches 77; Conservative 51; Mismatches 139; Indels 27; Gaps 7;

QY 12 FLAGVAAAIKSTAVAPIERVTLLOVQHASKQITADKQYKGIIDCVRIPEQEVLSFW 71
DB 104 FGLSVAGVAGTAVYPIDLVKTMMQNRSTGSPFGLMKNKNSPDCFKVLRYSGEFFGLY 163
QY 72 RGNLANVIRYPTQALNPAFKDKYKQIFL---GGVDKRTQFRRYAGNLASGGAAGATSL 128
DB 164 RGLLPOLLGVAPEKAIKLTVDNFVRDKFMHKGVSVP-----LAABEILAGGCGAGGSQV 215
QY 129 CFVYPLDPAFRLADVGKAGAREFRGLDCLVIYKSDGKGLYOGFNVSVQGI 188
DB 216 IFTMPLELVKIRLQV-----AGEITTPRVSALSVARDLGFPGIYKAKACFLDIPFS 269
QY 189 AAYFGIYDTAKGMLDPPKXTHIVISWMLAQVTAVAGLTS---YPPDVRMMQSGR 244
DB 270 AIVFCYAHVAKASPNEDQGVSPGSLLLA---GALAGMPASLVTPADVIKTR--LQVAA 324
QY 245 KGTIMTGTILDCMRKIADDEGKAFPKGAMSVNLRMGCG-AFVLVLYDEIKKY 297

DB 325 RAGQTTYSVIDCPRKILREBGPALMKAGARVFRSSPQGVTLITYELLQRW 378

RESULT 11
US-09-160-119-2
Sequence 2, Application US/09160119A
Patent No. 6316219

GENERAL INFORMATION:
APPLICANT: KRIEF, STEPHANE
APPLICANT: SOUCHET, MICHEL
APPLICANT: BRIL, ANTOINE
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30985
CURRENT APPLICATION NUMBER: US/09/160,119A
CURRENT FILING DATE: 1998-09-24
EARLIER APPLICATION NUMBER: EP 97402511.6
EARLIER FILING DATE: 1997-10-23
EARLIER APPLICATION NUMBER: EP 98401655.0
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 674
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-160-119-2

Query Match 16.9%; Score 261.5; DB 4; Length 674;
Best Local Similarity 26.2%; Pred. No. 4, 4e-21;
Matches 77; Conservative 51; Mismatches 139; Indels 27; Gaps 7;

QY 12 FLAGVAAAIKSTAVAPIERVTLLOVQHASKQITADKQYKGIIDCVRIPEQEVLSFW 71
DB 331 FGLSVAGVAGTAVYPIDLVKTMMQNRSTGSPFGLMKNKNSPDCFKVLRYSGEFFGLY 390
QY 72 RGNLANVIRYPTQALNPAFKDKYKQIFL---GGVDKRTQFRRYAGNLASGGAAGATSL 128
DB 391 RGLLPOLLGVAPEKAIKLTVDNFVRDKFMHKGVSVP-----LAABEILAGGCGAGGSQV 442
QY 129 CFVYPLDPAFRLADVGKAGAREFRGLDCLVIYKSDGKGLYOGFNVSVQGI 188
DB 443 IFTMPLELVKIRLQV-----AGEITTPRVSALSVARDLGFPGIYKAKACFLDIPFS 496
QY 189 AAYFGIYDTAKGMLDPPKXTHIVISWMLAQVTAVAGLTS---YPPDVRMMQSGR 244
DB 497 AIVFCYAHVAKASPNEDQGVSPGSLLLA---GALAGMPASLVTPADVIKTR--LQVAA 551
QY 245 KGTIMTGTILDCMRKIADDEGKAFPKGAMSVNLRMGCG-AFVLVLYDEIKKY 297
DB 552 RAGQTTYSVIDCPRKILREBGPALMKAGARVFRSSPQGVTLITYELLQRW 605

RESULT 12
US-09-142-565-2
Sequence 2, Application US/09142565A
Patent No. 6187560

GENERAL INFORMATION:
APPLICANT: Lee James Beeley
APPLICANT: Kelly Paine
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30002
CURRENT APPLICATION NUMBER: US/09/142,565A
CURRENT FILING DATE: 1999-06-30
EARLIER APPLICATION NUMBER: 9704551.2
EARLIER FILING DATE: 1997-03-05
EARLIER APPLICATION NUMBER: 9705614.7
EARLIER FILING DATE: 1997-03-18
EARLIER APPLICATION NUMBER: 97305305.1
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2
LENGTH: 312
TYPE: PRT
ORGANISM: HOMO SAPIEN
US-09-142-565-2

Query Match 16.0%; Score 247; DB 3; Length 312;
Best Local Similarity 24.8%; Pred. No. 6, 2e-20;
Matches 76; Conservative 56; Mismatches 149; Indels 26; Gaps 8;

QY 2 TDALSPADFLAGVAIAISTAVAPIERVLILQVHASKQITADK--QYKGIIDCV 59
DB 7 SDVPMTAVKFLGATGACFADLTVPDLTAKVRLIQIENQAVQTARLVQRYGLTIL 66
QY 60 RLPKQEVLSFRGNLANVIRPPTQALNFAKDKKQIFL--GSVDKRTQFRYAGNLA 118
DB 67 TMRVTEGSPGPNGLVAGIQRMSPASIRIGLYDSVKQVYTPKGDNSLTTRILA---- 122
QY 119 SGGAAGATSLCFVYPLDFARTLADV--GKAGAREPFGLDCLVKIKYSDIKGLXQG 176
DB 123 -GCTGAAAVTCAQPTDVVKVAFQASIHGSPRSRDKSGTMDAYRTTAREGVGLWKG 181
QY 177 FNVSVQGIILYRAVFGIYDTAK-----GMLPDPKATHIVISWMLAQTVTAAGLTSP 230
DB 182 TLPTNIRNAIVNCAEVVTYDILKEKLDVHLLTDNPFCHVSAFGAGFCATVVAS----P 237
QY 231 PTVRRMMQSGRGTDMITGTLDCWKRIARDGGAFFKGMANSVLR--GMGAPVLV 289
DB 238 VDVVTRVY-----NSPPQGYSPIDCMIKVAQSGPTAFYKGTPTSLRLQSNVNVFV 292
QY 290 LYDEIKK 296
DB 293 TYEQAKR 299

RESULT 13

US-08-775-009-33
Sequence 33, Application US/08775009
Patent No. 5935783

GENERAL INFORMATION:
APPLICANT: Gong, Wellong
APPLICANT: Emanuel, Beverly S.
APPLICANT: Budarf, Marcia L.
APPLICANT: Roe, Bruce
TITLE OF INVENTION: No. 5935783el Genes Mapping in the Digestion and
TITLE OF INVENTION: Velocardiofacial Syndrome Minimal Critical Region
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESS: Woodcock Washburn Kurtz Mackiewicz &
ADDRESS: No. 5935783is, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/775,009
FILING DATE: 27-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yalko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CH-0681
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:

LENGTH: 311 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-775-009-33

Query Match 15.8%; Score 244.5; DB 2; Length 311;
Best Local Similarity 28.1%; Pred. No. 1, 2e-19;
Matches 83; Conservative 47; Mismatches 138; Indels 27; Gaps 8;

QY 10 KDPLAGVAAIAISTAVAPIERVLILQVHASKQITADKQYKGIIDCVNIPKQEVLS 69
DB 27 KAILAGLAGIIEICITPTETVYKQLQDLERAN-----PPRIKIGDCVRRYVSHGLG 82
QY 70 FMRGNLANVIRPPTQALNFA--PKQYKQIFLAGVDKRTQFMRYPAGNLAGGAAGAT 126
DB 83 LYRGISILYSGISIPAAVRFQMFPEFLSNHMDAQGRILDSR-----RGLLCGLAGVAB 135
QY 127 SLCPVYPLDFARTLADVAGKAGAREPFGLDCLVKIKYSDIKGLYQGFNVSVQGIIL 186
DB 136 AVVVVCEPMTVKVFIHD--QTSNPKYRPFHGVREIVRQGLKGYQLATVLYKQGS 193
QY 187 YRAVFGIYDTAKGMLPDPKATHIVISWMLAQTVTAAGLTSP-----PFDTVRRMMQGS 242
DB 194 NQAIRPFWMTSLRWY--QGDNPKNPNPLINGVGAAGAASVGNTPLDVITKRMQGLE 252
QY 243 GRKGTDMITGTLDCWKRIARDGGAFFKGMANSVLR--GMGAPVLVLYDEIKK 296
DB 253 AHK-----YRNTLDGVOILKNEGPKAFYKGTVPRLGVCDAIVFVYIDEVAK 302

RESULT 14

US-08-518-878B-51
Sequence 51, Application US/08518878B
Patent No. 5702302

GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/518,878B
FILING DATE: 23-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-518-878B-51

Query Match 15.5%; Score 239.5; DB 1; Length 309;
 Best Local Similarity 23.5%; Pred. No. 4.4e-19;
 Matches 72; Conservative 58; Mismatches 149; Indels 27; Gaps 8;

2 TDAALSPADFLAGGAAAIKSTAVAPIERVKLLLOVQHASK---QITADKQYKGIIDCV 58
 7 TDVPTATVTKELGAGTACIADLITFPLDTAKVRLQIGESGQPVRAIVSAQYGVWGII 66
 59 VRIPEQEVLSFWRGNLANVIRYPTQALNFAFKQYKQIFLGVDKRTQWRRYAGNLA 118
 67 LTMVTEGPRSLYNGLVAGLQROMSPASVRIGLYDSVKQFYTKGSEHAS-----IGSRL 121
 119 SGGAAGATSLCFVYPLDPAFRLADVKGAGAREFRGIDCLVIKYSDDGKIGLYOGFN 178
 122 AGSTTGALAVAVAQPTDVVKYRFQAO-ARAGGRRYQSTVNAKYTIAREBEGFRGLMKGTS 180
 179 VSVGGIITIRAYFGIYDTAK-----GMLPDPKNTHTIVISMMIAQTVAVAGLTSYFPD 232
 181 PNVARNNAIVNCABELVYDILKDALIKANLMTDDLPCFTSAFGAGFCTTVIAS----PVD 236
 233 TVRRMMMQS-GRKGTDMYTGTLDCWRKIARDEGKAFKFGAMSNTLR-GMGAFVLYL 290
 237 VKTRRYMSALGQ-----YSSAGHCALTMLQKEGPRAFYKGFMPSPFLRGSNNVVMFVT 290
 291 YDEIKK 296
 291 YEQLKR 296

RESULT 15
 US-08-807-861A-51
 ; Sequence 51, Application US/08807861A
 ; Patent No. 5853975

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE

NUMBER OF SEQUENCES: 64 REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY

CORRESPONDENCE ADDRESS:

ADDRESSER: Pennie & Edmonds LLP

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/807,861A

FILING DATE: 26-FEB-1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/518,878

FILING DATE: 23-AUG-1995

APPLICATION NUMBER: US 08/470,868

FILING DATE: 06-JUN-1995

APPLICATION NUMBER: US 08/294,522

FILING DATE: 23-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-066

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:

LENGTH: 309 amino acids

TYPE: amino acid

STRANDEDNESS: single
 ;
 ; TOPOLOGY: unknown
 ;
 ; US-08-807-861A-51

Query Match 15.5%; Score 239.5; DB 2; Length 309;
 Best Local Similarity 23.5%; Pred. No. 4.4e-19;
 Matches 72; Conservative 58; Mismatches 149; Indels 27; Gaps 8;

2 TDAALSPADFLAGGAAAIKSTAVAPIERVKLLLOVQHASK---QITADKQYKGIIDCV 58
 7 TDVPTATVTKELGAGTACIADLITFPLDTAKVRLQIGESGQPVRAIVSAQYGVWGII 66
 59 VRIPEQEVLSFWRGNLANVIRYPTQALNFAFKQYKQIFLGVDKRTQWRRYAGNLA 118
 67 LTMVTEGPRSLYNGLVAGLQROMSPASVRIGLYDSVKQFYTKGSEHAS-----IGSRL 121
 119 SGGAAGATSLCFVYPLDPAFRLADVKGAGAREFRGIDCLVIKYSDDGKIGLYOGFN 178
 122 AGSTTGALAVAVAQPTDVVKYRFQAO-ARAGGRRYQSTVNAKYTIAREBEGFRGLMKGTS 180
 179 VSVGGIITIRAYFGIYDTAK-----GMLPDPKNTHTIVISMMIAQTVAVAGLTSYFPD 232
 181 PNVARNNAIVNCABELVYDILKDALIKANLMTDDLPCFTSAFGAGFCTTVIAS----PVD 236
 233 TVRRMMMQS-GRKGTDMYTGTLDCWRKIARDEGKAFKFGAMSNTLR-GMGAFVLYL 290
 237 VKTRRYMSALGQ-----YSSAGHCALTMLQKEGPRAFYKGFMPSPFLRGSNNVVMFVT 290
 291 YDEIKK 296
 291 YEQLKR 296

Search completed: December 18, 2003, 12:44:55
 Job time: 13.3471 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:43:17 ; Search time 24.3606 Seconds
(without alignments)
2284.595 Million cell updates/sec

Title: US-09-811-131-32

Perfect score: 1547

Sequence: 1 MTDAALSPADFLAGVAA.....LRGNGAFVLVDEIKKKT 298

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1547	100.0	298	9	US-09-811-094-32
2	1547	100.0	298	9	US-09-810-644-32
3	1547	100.0	298	10	US-09-185-904A-32
4	1454	94.0	298	9	US-09-811-094-33
5	1454	94.0	298	9	US-09-810-644-33
6	1454	94.0	298	10	US-09-185-904A-33
7	1391.5	89.9	297	9	US-09-811-094-31
8	1391.5	89.9	297	9	US-09-810-644-31
9	1391.5	89.9	297	10	US-09-185-904A-31
10	840	54.3	179	12	US-10-029-386-32501
11	779.5	50.4	301	12	US-10-032-585-7194
12	752.5	48.6	318	10	US-09-801-368-252
13	741.5	47.9	381	12	US-10-141-478A-2
14	741.5	47.9	386	9	US-09-734-559-170
15	734	47.4	308	15	US-10-128-714-3338

16	734	47.4	308	15	US-10-128-714-8338	Sequence 8338, Ap
17	677.5	43.8	677	12	US-10-259-165-192	Sequence 192, Ap
18	484	31.3	132	9	US-09-925-301-1459	Sequence 1459, Ap
19	448	29.0	87	9	US-09-864-761-36440	Sequence 36440, A
20	351	22.7	477	10	US-09-777-921A-2	Sequence 2, Appl1
21	350	22.6	475	10	US-09-777-921A-4	Sequence 4, Appl1
22	323.5	20.9	410	10	US-09-777-921A-5	Sequence 5, Appl1
23	309	20.0	384	12	US-10-094-749-1789	Sequence 1789, Ap
24	302	19.5	469	9	US-09-989-722-289	Sequence 289, Ap
25	302	19.5	469	9	US-09-989-723-289	Sequence 289, Ap
26	302	19.5	469	9	US-09-989-279-289	Sequence 289, Ap
27	302	19.5	469	9	US-09-989-727-289	Sequence 289, Ap
28	302	19.5	469	10	US-09-989-731-289	Sequence 289, Ap
29	302	19.5	469	10	US-09-989-732-289	Sequence 289, Ap
30	302	19.5	469	10	US-09-991-073-289	Sequence 289, Ap
31	302	19.5	469	10	US-09-991-163-289	Sequence 289, Ap
32	302	19.5	469	10	US-09-991-163-289	Sequence 289, Ap
33	302	19.5	469	10	US-09-993-604-289	Sequence 289, Ap
34	302	19.5	469	10	US-09-990-456-289	Sequence 289, Ap
35	302	19.5	469	10	US-09-989-721-289	Sequence 289, Ap
36	302	19.5	469	10	US-09-992-598-289	Sequence 289, Ap
37	302	19.5	469	10	US-09-989-735-289	Sequence 289, Ap
38	302	19.5	469	10	US-09-989-735-289	Sequence 289, Ap
39	302	19.5	469	10	US-09-990-444-289	Sequence 289, Ap
40	302	19.5	469	10	US-09-991-181-289	Sequence 289, Ap
41	302	19.5	469	10	US-09-989-730-289	Sequence 289, Ap
42	302	19.5	469	10	US-09-990-436-289	Sequence 289, Ap
43	302	19.5	469	10	US-09-993-687-289	Sequence 289, Ap
44	302	19.5	469	11	US-09-989-734-289	Sequence 289, Ap
45	302	19.5	469	11	US-09-997-653-289	Sequence 289, Ap

ALIGNMENTS

RESULT 1

US-09-811-094-32

Sequence 32, Application US/09811094

Patent No. US2001004144A1

GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.

APPLICANT: Davis, Robert E.

APPLICANT: Clevenger, William

APPLICANT: Wiley, Sandra Eileen

APPLICANT: Willey, Scott W.

APPLICANT: Szabo, Tomas R.

APPLICANT: Ghosh, Soumitra S.

APPLICANT: Moos, Walter H.

APPLICANT: Pei, Yezhong

TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),

TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR

FILE REFERENCE: 660088.420D4

CURRENT APPLICATION NUMBER: US/09/811,094

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 32

LENGTH: 298

TYPE: PRT

ORGANISM: Homo sapien

US-09-811-094-32

Query Match 100.0%; Score 1547; DB 9; Length 298;

Best Local Similarity 100.0%; Pred. No. 6,6e-159;

Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTDAALSPADFLAGVAAISKRAVPIRRVLLLOVQASAKTIDKQYKGIIDCVR 60

DB 1 MTDAALSPADFLAGVAAISKRAVPIRRVLLLOVQASAKTIDKQYKGIIDCVR 60

OY 1PKQEVLSFPGKGLAVIRVPTQALNFAFKDKYKQIFGQVYDKTQFRYFAGNLAAG 120

DB 1PKQEVLSFPGKGLAVIRVPTQALNFAFKDKYKQIFGQVYDKTQFRYFAGNLAAG 120

QY 121 GAAGATSICTFYPLDPARTRLADYVKGAGAEERFGLDCLVKIKYSGIKGLYOGFNV 180
DB 121 GAAGATSICTFYPLDPARTRLADYVKGAGAEERFGLDCLVKIKYSGIKGLYOGFNV 180
QY 181 VGGIITRYAAAFGYIDTAKGMLPDKNTHIVISNMIAQTVAVAGLTSYPTVRRMM 240
DB 181 VGGIITRYAAAFGYIDTAKGMLPDKNTHIVISNMIAQTVAVAGLTSYPTVRRMM 240
QY 241 QSGRGTIDIMYTGTLDCWRKIARDGGAFFKGAMSNVLRGNGAFVLVLYDEIKKYT 298
DB 241 QSGRGTIDIMYTGTLDCWRKIARDGGAFFKGAMSNVLRGNGAFVLVLYDEIKKYT 298

RESULT 2
US-09-810-644-32
; Sequence 32, Application US/09810644
; Patent No. US20020012992A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Cleveenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Miller, Scott W.
; APPLICANT: Szabo, Thomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pel, Yazhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.420D3
; CURRENT APPLICATION NUMBER: US/09/810,644
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-810-644-32

Query Match 100.0%; Score 1547; DB 9; Length 298;
Best Local Similarity 100.0%; Pred. No. 6.6e-159;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKOITADKOYKGIIDCYVR 60
DB 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKOITADKOYKGIIDCYVR 60
QY 61 IPKEQEVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
DB 61 IPKEQEVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
QY 121 GAAGTSTICTFYPLDPARTRLADYVKGAGAEERFGLDCLVKIKYSGIKGLYOGFNV 180
DB 121 GAAGTSTICTFYPLDPARTRLADYVKGAGAEERFGLDCLVKIKYSGIKGLYOGFNV 180
QY 181 VGGIITRYAAAFGYIDTAKGMLPDKNTHIVISNMIAQTVAVAGLTSYPTVRRMM 240
DB 181 VGGIITRYAAAFGYIDTAKGMLPDKNTHIVISNMIAQTVAVAGLTSYPTVRRMM 240
QY 241 QSGRGTIDIMYTGTLDCWRKIARDGGAFFKGAMSNVLRGNGAFVLVLYDEIKKYT 298
DB 241 QSGRGTIDIMYTGTLDCWRKIARDGGAFFKGAMSNVLRGNGAFVLVLYDEIKKYT 298

RESULT 3
US-09-185-904A-32
; Sequence 32, Application US/09185904A
; Patent No. US2002017185A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.

APPLICANT: Cleveenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Miller, Scott W.
; APPLICANT: Szabo, Thomas R.
; APPLICANT: Ghosh, Soumitra S.
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
; TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
; FILE REFERENCE: 660088.420
; CURRENT APPLICATION NUMBER: US/09/185,904A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-185-904A-32

Query Match 100.0%; Score 1547; DB 10; Length 298;
Best Local Similarity 100.0%; Pred. No. 6.6e-159;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKOITADKOYKGIIDCYVR 60
DB 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKOITADKOYKGIIDCYVR 60
QY 61 IPKEQEVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
DB 61 IPKEQEVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
QY 121 GAAGTSTICTFYPLDPARTRLADYVKGAGAEERFGLDCLVKIKYSGIKGLYOGFNV 180
DB 121 GAAGTSTICTFYPLDPARTRLADYVKGAGAEERFGLDCLVKIKYSGIKGLYOGFNV 180
QY 181 VGGIITRYAAAFGYIDTAKGMLPDKNTHIVISNMIAQTVAVAGLTSYPTVRRMM 240
DB 181 VGGIITRYAAAFGYIDTAKGMLPDKNTHIVISNMIAQTVAVAGLTSYPTVRRMM 240
QY 241 QSGRGTIDIMYTGTLDCWRKIARDGGAFFKGAMSNVLRGNGAFVLVLYDEIKKYT 298
DB 241 QSGRGTIDIMYTGTLDCWRKIARDGGAFFKGAMSNVLRGNGAFVLVLYDEIKKYT 298

RESULT 4
US-09-811-094-33
; Sequence 33, Application US/09811094
; Patent No. US2001004414A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Cleveenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Miller, Scott W.
; APPLICANT: Szabo, Thomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pel, Yazhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.420D4
; CURRENT APPLICATION NUMBER: US/09/811,094
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-811-094-33

Query Match 94.0%; Score 1454; DB 9; Length 298;
Best Local Similarity 92.6%; Pred. No. 7.7e-149;

Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

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 DB 1 MTEQALSPAKDFLAGVAAIASTKAVAPIERVKLLQVQHASKOTIADKQYGIIDCVR 60
 QY 61 IPKEQEVLSFWRGNLANVIRYPTQALNFAFKDKTKQIFLGVDKRTQFWRFFAGNLASG 120
 DB 61 IPKEQGVLSFWRGNLANVIRYPTQALNFAFKDKTKQIFLGVDGHTQFWRFFAGNLASG 120
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 DB 121 GAAGATSLCFYYPDLPARTRLAADVGKSGTEREERGLDCLVKIKYSGIKGLYQGFVS 180
 QY 181 VGGIITRAAYFGYDTRAKGMLPDKNTHIYSMMIAQTVAVAGLSYPPDYRRRRMM 240
 DB 181 VGGIITRAAYFGYDTRAKGMLPDKNTHIYSMMIAQTVAVAGVSYPPDYRRRRMM 240
 QY 241 QSGRKGDTIMYTGTLDCWRKIARDGGAFFKGAANSVLRGMAFVLVLYDEIKK 296
 DB 241 QSGRGADIMYTGTVDCWRKIFRDEGGKAFKGAANSVLRGMAFVLVLYDELKX 296

RESULT 5
 US-09-810-644-33
 ; Sequence 33, Application US/09810644
 ; Patent No. US20020012992A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Christen M.
 ; APPLICANT: Davis, Robert E.
 ; APPLICANT: Clewenger, William
 ; APPLICANT: Wiley, Sandra Eileen
 ; APPLICANT: Miller, Scott W.
 ; APPLICANT: Szabo, Tomas R.
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Moos, Walter H.
 ; APPLICANT: Pei, Yazhong
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
 ; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
 ; FILE REFERENCE: 660088.420D3
 ; CURRENT APPLICATION NUMBER: US/09/810,644
 ; CURRENT FILING DATE: 2001-03-14
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 33
 ; LENGTH: 298
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-09-810-644-33

Query Match 94.0%; Score 1454; DB 9; Length 298;
 Best Local Similarity 92.6%; Pred. No. 7.7e-149;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTDALSPAKDFLAGVAAIASTKAVAPIERVKLLQVQHASKOTIADKQYGIIDCVR 60
 DB 1 MTEQALSPAKDFLAGVAAIASTKAVAPIERVKLLQVQHASKOTIADKQYGIIDCVR 60
 QY 61 IPKEQEVLSFWRGNLANVIRYPTQALNFAFKDKTKQIFLGVDKRTQFWRFFAGNLASG 120
 DB 61 IPKEQGVLSFWRGNLANVIRYPTQALNFAFKDKTKQIFLGVDGHTQFWRFFAGNLASG 120
 QY 121 GAAGATSLCFYYPDLPARTRLAADVGKAGAREBERGLDCLVKIKYSGIKGLYQGFVS 180
 DB 121 GAAGATSLCFYYPDLPARTRLAADVGKSGTEREERGLDCLVKIKYSGIKGLYQGFVS 180
 QY 181 VGGIITRAAYFGYDTRAKGMLPDKNTHIYSMMIAQTVAVAGLSYPPDYRRRRMM 240
 DB 181 VGGIITRAAYFGYDTRAKGMLPDKNTHIYSMMIAQTVAVAGVSYPPDYRRRRMM 240
 QY 241 QSGRKGDTIMYTGTLDCWRKIARDGGAFFKGAANSVLRGMAFVLVLYDEIKK 296
 DB 241 QSGRGADIMYTGTVDCWRKIFRDEGGKAFKGAANSVLRGMAFVLVLYDELKX 296

RESULT 6
 US-09-185-904A-33
 ; Sequence 33, Application US/09185904A
 ; Patent No. US20020177185A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Christen M.
 ; APPLICANT: Davis, Robert E.
 ; APPLICANT: Clewenger, William
 ; APPLICANT: Wiley, Sandra Eileen
 ; APPLICANT: Miller, Scott W.
 ; APPLICANT: Szabo, Tomas R.
 ; APPLICANT: Ghosh, Soumitra S.
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
 ; TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
 ; FILE REFERENCE: 660088.420
 ; CURRENT APPLICATION NUMBER: US/09/185,904A
 ; CURRENT FILING DATE: 1998-11-03
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 33
 ; LENGTH: 298
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-09-185-904A-33

Query Match 94.0%; Score 1454; DB 10; Length 298;
 Best Local Similarity 92.6%; Pred. No. 7.7e-149;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTDALSPAKDFLAGVAAIASTKAVAPIERVKLLQVQHASKOTIADKQYGIIDCVR 60
 DB 1 MTEQALSPAKDFLAGVAAIASTKAVAPIERVKLLQVQHASKOTIADKQYGIIDCVR 60
 QY 61 IPKEQEVLSFWRGNLANVIRYPTQALNFAFKDKTKQIFLGVDKRTQFWRFFAGNLASG 120
 DB 61 IPKEQGVLSFWRGNLANVIRYPTQALNFAFKDKTKQIFLGVDGHTQFWRFFAGNLASG 120
 QY 121 GAAGATSLCFYYPDLPARTRLAADVGKAGAREBERGLDCLVKIKYSGIKGLYQGFVS 180
 DB 121 GAAGATSLCFYYPDLPARTRLAADVGKSGTEREERGLDCLVKIKYSGIKGLYQGFVS 180
 QY 181 VGGIITRAAYFGYDTRAKGMLPDKNTHIYSMMIAQTVAVAGLSYPPDYRRRRMM 240
 DB 181 VGGIITRAAYFGYDTRAKGMLPDKNTHIYSMMIAQTVAVAGVSYPPDYRRRRMM 240
 QY 241 QSGRKGDTIMYTGTLDCWRKIARDGGAFFKGAANSVLRGMAFVLVLYDEIKK 296
 DB 241 QSGRGADIMYTGTVDCWRKIFRDEGGKAFKGAANSVLRGMAFVLVLYDELKX 296

RESULT 7
 US-09-811-094-31
 ; Sequence 31, Application US/09811094
 ; Patent No. US2001004414A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Christen M.
 ; APPLICANT: Davis, Robert E.
 ; APPLICANT: Clewenger, William
 ; APPLICANT: Wiley, Sandra Eileen
 ; APPLICANT: Miller, Scott W.
 ; APPLICANT: Szabo, Tomas R.
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Moos, Walter H.
 ; APPLICANT: Pei, Yazhong
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
 ; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
 ; FILE REFERENCE: 660088.420D4
 ; CURRENT APPLICATION NUMBER: US/09/811,094
 ; CURRENT FILING DATE: 2001-03-14
 ; NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 31
LENGTH: 297
TYPE: PRT
ORGANISM: Homo sapien
US-09-811-094-31

Query Match 89.9%; Score 1391.5; DB 9; Length 297;
Best Local Similarity 88.6%; Pred. No. 4.5e-142;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHSKQITADKQYGIIDCVR 60
DB 1 MGDHMSFLKDFLAQVAAVASKTAVAPIERVKLLQVQHSKQISAEKQYGIIDCVR 60
QY 61 IPKEQEVLSFWRGNLANIYRFPYPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120
DB 61 IPKEQGLISFWRGNLANIYRFPYPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120
QY 121 GAAGATSLCFYVPDLPARTRLAADVKGAKAEERFGLDCLVKIYKSDGKGLYGFVNS 180
DB 121 GAAGATSLCFYVPDLPARTRLAADVKGAKAEERFGLDCLVKIYKSDGKGLYGFVNS 179
QY 181 VGGIITRYAAAFYGYDPAKGMPLDPKNTHTIYSNMIAQTVAAGLTSYPTVRRRMM 240
DB 180 VGGIITRYAAAFYGYDPAKGMPLDPKNTHTIYSNMIAQSVAAGLTSYPTVRRRMM 239
QY 241 QSGRKGTDIMYTGTLDCWRKIARDGKAFKFGAMSNVLRGMGAFVLVLYDEIKKY 297
DB 240 QSGRKGADIMYTGTVDCWRKIARDGKAFKFGAMSNVLRGMGAFVLVLYDEIKKY 296

RESULT 8

US-09-810-644-31
Sequence 31, Application US/09810644
Patent No. US20020012992A1

GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Cleveland, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pel, Yashong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D3
CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 31
LENGTH: 297
TYPE: PRT
ORGANISM: Homo sapien
US-09-810-644-31

Query Match 89.9%; Score 1391.5; DB 9; Length 297;
Best Local Similarity 88.6%; Pred. No. 4.5e-142;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHSKQITADKQYGIIDCVR 60
DB 1 MGDHMSFLKDFLAQVAAVASKTAVAPIERVKLLQVQHSKQISAEKQYGIIDCVR 60
QY 61 IPKEQEVLSFWRGNLANIYRFPYPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120
DB 61 IPKEQGLISFWRGNLANIYRFPYPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120
QY 121 GAAGATSLCFYVPDLPARTRLAADVKGAKAEERFGLDCLVKIYKSDGKGLYGFVNS 180
DB 121 GAAGATSLCFYVPDLPARTRLAADVKGAKAEERFGLDCLVKIYKSDGKGLYGFVNS 180

DB 121 GAAGATSLCFYVPDLPARTRLAADVGR-AQREHFGLDCLIKIFKSDGLAGLYGFVNS 179
QY 181 VGGIITRYAAAFYGYDPAKGMPLDPKNTHTIYSNMIAQTVAAGLTSYPTVRRRMM 240
DB 180 VGGIITRYAAAFYGYDPAKGMPLDPKNTHTIYSNMIAQSVAAGLTSYPTVRRRMM 239
QY 241 QSGRKGTDIMYTGTLDCWRKIARDGKAFKFGAMSNVLRGMGAFVLVLYDEIKKY 297
DB 240 QSGRKGADIMYTGTVDCWRKIARDGKAFKFGAMSNVLRGMGAFVLVLYDEIKKY 296

RESULT 9

US-09-185-904A-31
Sequence 31, Application US/09185904A
Patent No. US20020177185A1

GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Cleveland, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 660088.420
CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 31
LENGTH: 297
TYPE: PRT
ORGANISM: Homo sapien
US-09-185-904A-31

Query Match 89.9%; Score 1391.5; DB 10; Length 297;
Best Local Similarity 88.6%; Pred. No. 4.5e-142;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHSKQITADKQYGIIDCVR 60
DB 1 MGDHMSFLKDFLAQVAAVASKTAVAPIERVKLLQVQHSKQISAEKQYGIIDCVR 60
QY 61 IPKEQEVLSFWRGNLANIYRFPYPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120
DB 61 IPKEQGLISFWRGNLANIYRFPYPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120
QY 121 GAAGATSLCFYVPDLPARTRLAADVKGAKAEERFGLDCLVKIYKSDGKGLYGFVNS 180
DB 121 GAAGATSLCFYVPDLPARTRLAADVGR-AQREHFGLDCLIKIFKSDGLAGLYGFVNS 179
QY 181 VGGIITRYAAAFYGYDPAKGMPLDPKNTHTIYSNMIAQTVAAGLTSYPTVRRRMM 240
DB 180 VGGIITRYAAAFYGYDPAKGMPLDPKNTHTIYSNMIAQSVAAGLTSYPTVRRRMM 239
QY 241 QSGRKGTDIMYTGTLDCWRKIARDGKAFKFGAMSNVLRGMGAFVLVLYDEIKKY 297
DB 240 QSGRKGADIMYTGTVDCWRKIARDGKAFKFGAMSNVLRGMGAFVLVLYDEIKKY 296

RESULT 10

US-10-029-386-32501
Sequence 32501, Application US/10029386
Publication No. US20030194704A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AROMICA-X-2

CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 32501
LENGTH: 179
TYPE: PR1
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC004000.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.95
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96
OTHER INFORMATION: SWISSPROT HIT: P05141, EVALU2 2.00e-83
US-10-029-386-32501

Query Match 54.3%; Score 840; DB 12; Length 179;
Best Local Similarity 98.8%; Pred. No. 1.1e-82;
Matches 161; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 38 VQHASKQITADKQYKGIIDCVRIPEQEVLSFMRGNLANVIRYPTQALNFAFKDKYKQ 97
DB 1 VQHASKQITADKQYKGIIDCVRIPEQEVLSFMRGNLANVIRYPTQALNFAFKDKYKQ 60

QY 98 IFPGVDKRTQPMRYFPAAGNLASGGAAGTSLCFYVPLDPATRLAADVGAERERFGL 157
DB 61 IFPGVDKRTQPMRYFPAAGNLASGGAAGTSLCFYVPLDPATRLAADVGAERERFGL 120

QY 158 GDCLVKIKSDIKGLYOGFNVSVGGIIRYAAVGIYDTAKG 200
DB 121 GDCLVKIKSDIKGLYOGFNVSVGGIIRYAAVGIYDTAKG 163

RESULT 11
US-10-032-585-7194
Sequence 7194, Application US/10032585
Publication No. US20030180953A1
GENERAL INFORMATION:
APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Charles, Bussey
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7194
LENGTH: 301
TYPE: PR1
ORGANISM: Candida albicans
US-10-032-585-7194

Query Match 50.4%; Score 779.5; DB 12; Length 301;
Best Local Similarity 54.5%; Pred. No. 8e-76;
Matches 163; Conservative 41; Mismatches 84; Indels 11; Gaps 6;

QY 1 MTDALSAKDFLAGVAAISKTAVAPIERVKLLIQVQ-HASKQITADKQYKGIIDCV 59
DB 1 MTDALSAKDFLAGVAAISKTAVAPIERVKLLIQVQ-HASKQITADKQYKGIIDCV 58

QY 60 RIPKEOVLSPMRGNLANVIRYPTQALNFAFKDKYKQIFPGVDKRTQPMRYFPAAGNLAS 119
DB 59 RTADEGVVSPMRGNLANVIRYPTQALNFAFKDKYKQIFPGVDKRTQPMRYFPAAGNLAS 116

QY 120 GGAAGATSLCFYVPLDPATRLAADV--GKAGAEERFGLGDCLVKIKSDIKGLYOGF 177
DB 117 GGLAGATSLAFYVPLDPATRLAADV--GKAGAEERFGLGDCLVKIKSDIKGLYOGF 176

QY 178 NVSVGGIIRYAAVGIYDTAKG-WLPPDKMTHIVISMIAQTVTAAGVLSYPPDITVR 236

DB 177 GPSVIGIVVRGLYFGIYDLSKPVLYVGPLEGSLAFILGMAVTTGASTASYLDITVR 236

QY 237 RMMQSGRKGTDMTGTTLDCMRKIADBGKAFKGAAGSVNLRGMGAFVLYIDEIK 295
DB 237 RMMQSGRKGTDMTGTTLDCMRKIADBGKAFKGAAGSVNLRGMGAFVLYIDEIK 292

RESULT 12
US-09-801-368-252
Sequence 252, Application US/09801368
Patent No. US20020128250A1
GENERAL INFORMATION:
APPLICANT: Bueby, Robert
APPLICANT: Call, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary
APPLICANT: Milne, Todd
APPLICANT: No. US20020128250A1man, Thea
APPLICANT: Royer, John
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: PatentIn version 3.0
SEQ ID NO 252
LENGTH: 318
TYPE: PR1
ORGANISM: Saccharomyces cerevisiae
US-09-801-368-252

Query Match 48.6%; Score 752.5; DB 10; Length 318;
Best Local Similarity 54.3%; Pred. No. 7.2e-73;
Matches 159; Conservative 40; Mismatches 85; Indels 9; Gaps 5;

QY 7 SPANDPLAGVAAISKTAVAPIERVKLLIQVQ-HASKQITADKQYKGIIDCVRIPEQ 65
DB 22 NPLDPLMGVSAVAATTAAPIERVKLLIQVQ-HASKQITADKQYKGIIDCVRIPEQ 81

QY 66 EVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFPGVDKRTQPMRYFPAAGNLASGGAAGA 125
DB 82 EVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFPGVDKRTQPMRYFPAAGNLASGGAAGA 139

QY 126 TSLCFYVPLDPATRLAAD--VGKAGAEERFGLGDCLVKIKSDIKGLYOGFNVSV 183
DB 140 TSLCFYVPLDPATRLAAD--VGKAGAEERFGLGDCLVKIKSDIKGLYOGFNVSV 199

QY 184 IIRYAAVGIYDTAKG-WLPPDKMTHIVISMIAQTVTAAGVLSYPPDITVR 242
DB 200 IIRYAAVGIYDTAKG-WLPPDKMTHIVISMIAQTVTAAGVLSYPPDITVR 259

QY 243 GRKTDIMTGTTLDCMRKIADBGKAFKGAAGSVNLRGMGAFVLYIDEIK 295
DB 260 GRKTDIMTGTTLDCMRKIADBGKAFKGAAGSVNLRGMGAFVLYIDEIK 309

RESULT 13
US-10-141-478A-2
Sequence 2, Application US/10141478A
Publication No. US20030148300A1
GENERAL INFORMATION:
APPLICANT: Valentín, Henry

APPLICANT: Savage, Thomas
APPLICANT: Voelker, Toni
APPLICANT: Zang, Wei
TITLE OF INVENTION: Metabolite Transporters
FILE REFERENCE: 16515.146
CURRENT APPLICATION NUMBER: US/10/141,478A
CURRENT FILING DATE: 2002-05-09
PRIOR APPLICATION NUMBER: US 60/289,519
PRIOR FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 60/289,527
PRIOR FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: To Be Assigned, Attorney Docket No. US20030148300A1: 16517.
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 381
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-141-478A-2

Query Match 47.9%; Score 741.5; DB 12; Length 381;
Best Local Similarity 53.6%; Pred. No. 1.4e-71;
Matches 165; Conservative 38; Mismatches 78; Indels 27; Gaps 8;

QY 7 SPADPLAGVAAAIKSTAVAPIERVKLLQVQHASQOITA--DKQYKGIIDCVVRIPK 63
DB NFALDFPLMGVSAVSAVSKTAAAPIERVKLLIQNQ--DEMIIKAGRLSEPKYKIGIDCFGRITK 136
QY 64 EGVLSFMRGNLNVIRYPTQALNPAFDKQYKIFLGVDKRTQFMVYPPGNLSSGAA 123
DB 137 DEGFSLMRGNLNVIRYPTQALNPAFDKQYKIFNFKQD--RDGYMKPFAGNLSSGAA 195
QY 124 GATSLCFVYPLDPAFRTLAAD---VGKAGAEERFRLGDCLVKIKYSDGIGLYOGFNVIS 180
DB 196 GASLFLFYSLDPAFRTLAADAKKAGGCGRQFGLVDVYKTKITGIGLYOGFNVIS 255
QY 181 VGGIIRYAAVFGIYDTAK---GMLDPKNTIIVISMIAGVTVAVAGLTSYFPDTR 235
DB 256 CVGIIVYGLVFGLYDSVYPLVLTGDLQSPFASPALGVV---TNGAGLASYPIDTVR 311
QY 226 RRMWMSGRKGDIMYTGTLDCWKRIARDEGKAFPKAMSVNLRGMGAPVLYVYDI- 294
DB 312 RRMWMTSMEA--VKYKSLDAFKQILNKGAKSLFKAGANILRAVAGVLSGYDKLT 368
QY 295 -----KKY 297
DB 369 LIVEKKY 376

RESULT 14
US-09-734-569-170
Sequence 170, Application US/09734569
Patent No. US20020064816A1
GENERAL INFORMATION:
APPLICANT: Lertch, Jens
APPLICANT: Renz, Andreas
APPLICANT: Ehrhardt, Thomas
APPLICANT: Reindl, Andreas
APPLICANT: Cirus, Petra
APPLICANT: Bischoff, Friedrich
APPLICANT: Frank, Markus
APPLICANT: Freund, Annette
APPLICANT: Duwendt, Elke
APPLICANT: Schmidt, Ralf-Michael
APPLICANT: Reek, Ralf

TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved
TITLE OF INVENTION: In the synthesis of carbohydrates
FILE REFERENCE: BASF-NAE-1332-99-US
CURRENT APPLICATION NUMBER: US/09/734,569
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/171,101
PRIOR FILING DATE: 1999-12-16

NUMBER OF SEQ ID NOS: 181
SOFTWARE: Patentin Ver. 2.1/WordPerfect 6.1
SEQ ID NO 170
LENGTH: 386
TYPE: PRT
ORGANISM: Physcomitrella patens
US-09-734-569-170

Query Match 47.9%; Score 741.5; DB 9; Length 386;
Best Local Similarity 53.4%; Pred. No. 1.5e-71;
Matches 157; Conservative 42; Mismatches 86; Indels 9; Gaps 5;

QY 7 SPADPLAGVAAAIKSTAVAPIERVKLLQVQHASQOITA--DKQYKGIIDCVVRIPK 65
DB 84 SFMTDFLMGVSAVSAVSKTAAAPIERVKLLIQNDEMILSGRLSHPKYKIGCFSTRVDE 143
QY 66 EVLSPMRGNLNVIRYPTQALNPAFDKQYKIFLGVDKRTQFMVYPPGNLSSGAA 125
DB 144 GMSLMRGNLNVIRYPTQALNPAFDKQYKIFLSL-GRYKQDQYKMFAGNLSSGAA 202
QY 126 TSLCFVYPLDPAFRTLAADV---GKAGAEERFRLGDCLVKIKYSDGIGLYOGFNVIS 182
DB 203 SSLFLFYSLDPAFRTLAADAKSKGCGRQFGLVDVYKTKITGIGLYOGFNVIS 262
QY 183 GIIRYAAVFGIYDTAK--MLPDKNTIIVISMIAGVTVAVAGLTSYFPDTR 241
DB 263 GIIVYGLVFGIYSLRVVYVGNLBNFLASFLGWTGITTGAGIASYPIDTVRRMMT 322
QY 242 SGRKGTDMYTGTLDCWKRIARDEGKAFPKAMSVNLRGMGAPVLYVYDIK 295
DB 323 SGRA---VKYKSLDAFKQILNKGAKSLFKAGANILRAVAGVLSGYDQ 373

RESULT 15
US-10-128-714-3338
Sequence 3338, Application US/10128714
Publication No. US20030119013A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Hu, Wenqi
APPLICANT: Liabkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Erobkhin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: Patentin version 3.1
SEQ ID NO 3338
LENGTH: 308
TYPE: PRT
ORGANISM: Aspergillus fumigatus
US-10-128-714-3338

Query Match 47.4%; Score 734; DB 15; Length 308;
Best Local Similarity 53.2%; Pred. No. 6.9e-71;
Matches 157; Conservative 41; Mismatches 85; Indels 12; Gaps 6;

QY 7 SPADPLAGVAAAIKSTAVAPIERVKLLQVQHASQOITA--DKQYKGIIDCVVRIPK 63
DB 157

```

Db      7 AFTDSFVAVGVSAVSKTAAPIERIKL--VQNDENIRAGRLDRKXNGIIDCFRRTAQ 64
Qy      64 BOEVLSPWRGNLANVIRYPTQALNFAFKDKYKOIFLGVDKRTQFWRYFAGNLASGGA 123
Db      65 AEGVMSLRGNLANVIRYPTQALNFAFKDKYKQD-RDGYAKMMGNLASGGA 123
Qy      124 GATSLCPYVPLDPARTRLAADV--GKAGAREFRGLDCLVKIKSDGIKGLYQGFNVSV 181
Db      124 GATSLLPYSLDYARTRLANDAKSAGGGERQFNGLIDVYRKTILASDGIAGLYRGFPSPV 183
Qy      182 OGIIIRAYRGIYDTAKG-MLPDPKTHIVISMIAQTVTAAGLTSPDPTRRRMM 240
Db      184 LGIVVYRGVFGMYDSIKPVVYVGSLEGSFLASFLGWTVTGAGIASYPLDTIRRRMM 243
Qy      241 OSGRGTIDIMYGTLDGWRKLTARDEGKAFKGAWSNLRGSGAFVLYDEIK 295
Db      244 TSGEA---VKYKSLDAARQITAKEGVKSLFKGAGANILRGVAGVLSIYDQV 295

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Search completed: December 18, 2003, 12:55:43
 Job time : 24.3606 secs

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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:40:52 ; Search time 165.852 Seconds
(without alignments)
1634.924 Million cell updates/sec

Title: US-09-811-131-32

Perfect score: 1547
Sequence: 1 MTDAALSPAKFLAGVAA.....LRGNGAFVLYVDEIKYT 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents AA Main:*

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2: /cgn2_6/ptodata/1/paa/US06_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*
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6: /cgn2_6/ptodata/1/paa/US082_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US083_COMB.pep:*
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9: /cgn2_6/ptodata/1/paa/US085_COMB.pep:*
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24: /cgn2_6/ptodata/1/paa/US099A_COMB.pep:*
25: /cgn2_6/ptodata/1/paa/US099B_COMB.pep:*
26: /cgn2_6/ptodata/1/paa/US100_COMB.pep:*
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32: /cgn2_6/ptodata/1/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1547	100.0	298	1	PCT-US01-15416-32 Sequence 32, Appl

2	1547	100.0	298	15	US-09-185-904A-32	Sequence 32, Appl
3	1547	100.0	298	17	US-09-393-441-32	Sequence 32, Appl
4	1547	100.0	298	21	US-09-709-785-48	Sequence 42, Appl
5	1547	100.0	298	23	US-09-809-827-32	Sequence 32, Appl
6	1547	100.0	298	23	US-09-809-889-32	Sequence 32, Appl
7	1547	100.0	298	23	US-09-810-644-32	Sequence 32, Appl
8	1547	100.0	298	23	US-09-811-094-32	Sequence 32, Appl
9	1547	100.0	298	23	US-09-811-132-32	Sequence 32, Appl
10	1537	99.4	298	1	PCT-US02-01048-54	Sequence 54, Appl
11	1537	99.4	298	19	US-09-569-327-5	Sequence 5, Appl
12	1537	99.4	298	10	US-10-466-162-54	Sequence 54, Appl
13	1537	99.4	298	32	US-09-452-680-20286	Sequence 20286, A
14	1537	99.4	332	22	US-09-760-469-1767	Sequence 1767, Ap
15	1537	99.4	332	28	US-10-216-583-1767	Sequence 1767, Ap
16	1530	98.9	298	30	US-10-408-765A-1631	Sequence 1631, Ap
17	1530	98.9	298	32	US-09-389-987-1631	Sequence 1631, Ap
18	1530	98.9	298	32	US-09-412-418-1631	Sequence 1631, Ap
19	1530	98.9	320	22	US-09-760-469-1310	Sequence 1310, Ap
20	1530	98.9	320	28	US-10-216-583-1310	Sequence 1310, Ap
21	1454	94.0	298	1	PCT-US01-15416-32	Sequence 33, Appl
22	1454	94.0	298	15	US-09-185-904A-33	Sequence 33, Appl
23	1454	94.0	298	17	US-09-393-441-33	Sequence 33, Appl
24	1454	94.0	298	18	US-09-488-725A-2786	Sequence 2786, Ap
25	1454	94.0	298	19	US-09-569-327-6	Sequence 6, Appl
26	1454	94.0	298	21	US-09-709-785-49	Sequence 49, Appl
27	1454	94.0	298	23	US-09-809-827-33	Sequence 33, Appl
28	1454	94.0	298	23	US-09-809-889-33	Sequence 33, Appl
29	1454	94.0	298	23	US-09-810-644-33	Sequence 33, Appl
30	1454	94.0	298	23	US-09-811-094-33	Sequence 33, Appl
31	1454	94.0	298	23	US-09-811-132-33	Sequence 33, Appl
32	1454	94.0	298	28	US-10-258-898A-2786	Sequence 2786, Ap
33	1454	94.0	298	28	US-10-286-897-2786	Sequence 2786, Ap
34	1454	94.0	323	18	US-09-488-725A-6358	Sequence 6358, Ap
35	1454	94.0	323	28	US-10-258-898A-6358	Sequence 6358, Ap
36	1454	94.0	323	28	US-10-286-897-6358	Sequence 6358, Ap
37	1450	93.7	298	30	US-10-403-571-154	Sequence 154, App
38	1450	93.7	298	30	US-10-405-887-154	Sequence 154, App
39	1448	93.6	298	30	US-10-408-765A-2398	Sequence 2398, Ap
40	1448	93.6	298	32	US-09-389-987-2398	Sequence 2398, Ap
41	1448	93.6	298	32	US-09-412-418-2398	Sequence 2398, Ap
42	1417	91.6	325	1	PCT-US01-08631-45782	Sequence 45782, A
43	1413	91.3	298	30	US-10-408-765A-1680	Sequence 1680, Ap
44	1413	91.3	298	32	US-09-389-987-1680	Sequence 1680, Ap
45	1413	91.3	298	32	US-09-412-418-1680	Sequence 1680, Ap

ALIGNMENTS

RESULT 1
PCT-US01-15416-32
Sequence 32, Application PC/RUS0115416
GENERAL INFORMATION:
APPLICANT: Micokor
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Willey, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
FILE REFERENCE: 660088.443PC
CURRENT APPLICATION NUMBER: PCT/US01/15416
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien

PCT-US01-15416-32

Query Match 100.0%; Score 1547; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.9e-159;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKOITADQYKGIIDCVR 60
DB 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKOITADQYKGIIDCVR 60
QY 1PKQEVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120
DB 1PKQEVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120
QY 121 GAAGATSLCFYVPLDPARTRLAADVGKAGAEERFGLDCLVKIKYSDGKGLYOGFNVS 180
DB 121 GAAGATSLCFYVPLDPARTRLAADVGKAGAEERFGLDCLVKIKYSDGKGLYOGFNVS 180
QY 161 VGGIIYRAAYFGIYDTAKGMLPDPKNTHTIVISWMIAGTVTAAGLTSYPPDYRRRRMM 240
DB 161 VGGIIYRAAYFGIYDTAKGMLPDPKNTHTIVISWMIAGTVTAAGLTSYPPDYRRRRMM 240
QY 241 QSGRGTIDIMYTGTLDCWRKIARDGGAFFKAGMSNVLRGMGAFVLVLYDEIKKTT 298
DB 241 QSGRGTIDIMYTGTLDCWRKIARDGGAFFKAGMSNVLRGMGAFVLVLYDEIKKTT 298

RESULT 2

US-09-185-904A-32

Sequence 32, Application US/09185904A

GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
FILE REFERENCE: 660088.420
CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-185-904A-32

Query Match 100.0%; Score 1547; DB 15; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.9e-159;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKOITADQYKGIIDCVR 60
DB 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKOITADQYKGIIDCVR 60
QY 61 1PKQEVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120
DB 61 1PKQEVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120
QY 121 GAAGATSLCFYVPLDPARTRLAADVGKAGAEERFGLDCLVKIKYSDGKGLYOGFNVS 180
DB 121 GAAGATSLCFYVPLDPARTRLAADVGKAGAEERFGLDCLVKIKYSDGKGLYOGFNVS 180
QY 161 VGGIIYRAAYFGIYDTAKGMLPDPKNTHTIVISWMIAGTVTAAGLTSYPPDYRRRRMM 240
DB 161 VGGIIYRAAYFGIYDTAKGMLPDPKNTHTIVISWMIAGTVTAAGLTSYPPDYRRRRMM 240
QY 241 QSGRGTIDIMYTGTLDCWRKIARDGGAFFKAGMSNVLRGMGAFVLVLYDEIKKTT 298
DB 241 QSGRGTIDIMYTGTLDCWRKIARDGGAFFKAGMSNVLRGMGAFVLVLYDEIKKTT 298

DB 241 QSGRGTIDIMYTGTLDCWRKIARDGGAFFKAGMSNVLRGMGAFVLVLYDEIKKTT 298

RESULT 3

US-09-393-441-32

Sequence 32, Application US/09393441
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yezhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420C1
CURRENT APPLICATION NUMBER: US/09/393,441
CURRENT FILING DATE: 1999-09-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-393-441-32

Query Match 100.0%; Score 1547; DB 17; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.9e-159;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKOITADQYKGIIDCVR 60
DB 1 MTDALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKOITADQYKGIIDCVR 60
QY 61 1PKQEVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120
DB 61 1PKQEVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120
QY 121 GAAGATSLCFYVPLDPARTRLAADVGKAGAEERFGLDCLVKIKYSDGKGLYOGFNVS 180
DB 121 GAAGATSLCFYVPLDPARTRLAADVGKAGAEERFGLDCLVKIKYSDGKGLYOGFNVS 180
QY 161 VGGIIYRAAYFGIYDTAKGMLPDPKNTHTIVISWMIAGTVTAAGLTSYPPDYRRRRMM 240
DB 161 VGGIIYRAAYFGIYDTAKGMLPDPKNTHTIVISWMIAGTVTAAGLTSYPPDYRRRRMM 240
QY 241 QSGRGTIDIMYTGTLDCWRKIARDGGAFFKAGMSNVLRGMGAFVLVLYDEIKKTT 298
DB 241 QSGRGTIDIMYTGTLDCWRKIARDGGAFFKAGMSNVLRGMGAFVLVLYDEIKKTT 298

RESULT 4

US-09-709-785-48

Sequence 48, Application US/09709785

GENERAL INFORMATION:
APPLICANT: Murphy, Anne N.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Frigeri, Luciano G.
APPLICANT: Velicelcbl, Gonul
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
FILE REFERENCE: 660088.433C1
CURRENT APPLICATION NUMBER: US/09/709,785
CURRENT FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 57

SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-709-785-48

Query Match 100.0%; Score 1547; DB 21; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.9e-159;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDAAISPAKDFLAGGVAIAISKTAVAPIERVKLLQVQHASKOITADKQKGIIDCVR 60
DB 1 MTDAAISPAKDFLAGGVAIAISKTAVAPIERVKLLQVQHASKOITADKQKGIIDCVR 60
QY 61 IPKQEVLSFMRGNLANIRYFPQALNFAFDKXKOIFLGVDKRTQFMRYPFAGNLASG 120
DB 61 IPKQEVLSFMRGNLANIRYFPQALNFAFDKXKOIFLGVDKRTQFMRYPFAGNLASG 120
QY 121 GAAGATSLCFYYPPLDFAFTRLAADVGAAGAREBERGGLDCLVKIKYSDGKGLYQGFNV 180
DB 121 GAAGATSLCFYYPPLDFAFTRLAADVGAAGAREBERGGLDCLVKIKYSDGKGLYQGFNV 180
QY 181 VGGIIRAAVFGIYDTAKGMLPDPKNTHTIVISWMIQVTAVALTSYFPDTRRRMM 240
DB 181 VGGIIRAAVFGIYDTAKGMLPDPKNTHTIVISWMIQVTAVALTSYFPDTRRRMM 240
QY 241 QSGRKGTDIMYTGTLDCWRKIARDEGGAFFKGAWSNVLKMGCAFVLVYDEIKK 298
DB 241 QSGRKGTDIMYTGTLDCWRKIARDEGGAFFKGAWSNVLKMGCAFVLVYDEIKK 298

RESULT 5

US-09-809-827-32
; Sequence 32, Application US/09809827
; GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pel, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D6
CURRENT APPLICATION NUMBER: US/09/809,827
CURRENT FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-809-827-32

Query Match 100.0%; Score 1547; DB 23; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.9e-159;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDAAISPAKDFLAGGVAIAISKTAVAPIERVKLLQVQHASKOITADKQKGIIDCVR 60
DB 1 MTDAAISPAKDFLAGGVAIAISKTAVAPIERVKLLQVQHASKOITADKQKGIIDCVR 60
QY 61 IPKQEVLSFMRGNLANIRYFPQALNFAFDKXKOIFLGVDKRTQFMRYPFAGNLASG 120
DB 61 IPKQEVLSFMRGNLANIRYFPQALNFAFDKXKOIFLGVDKRTQFMRYPFAGNLASG 120
QY 121 GAAGATSLCFYYPPLDFAFTRLAADVGAAGAREBERGGLDCLVKIKYSDGKGLYQGFNV 180
DB 121 GAAGATSLCFYYPPLDFAFTRLAADVGAAGAREBERGGLDCLVKIKYSDGKGLYQGFNV 180

QY 161 VGGIIRAAVFGIYDTAKGMLPDPKNTHTIVISWMIQVTAVALTSYFPDTRRRMM 240
DB 161 VGGIIRAAVFGIYDTAKGMLPDPKNTHTIVISWMIQVTAVALTSYFPDTRRRMM 240
QY 241 QSGRKGTDIMYTGTLDCWRKIARDEGGAFFKGAWSNVLKMGCAFVLVYDEIKK 298
DB 241 QSGRKGTDIMYTGTLDCWRKIARDEGGAFFKGAWSNVLKMGCAFVLVYDEIKK 298

RESULT 6

US-09-809-889-32
; Sequence 32, Application US/09809889
; GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pel, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D7
CURRENT APPLICATION NUMBER: US/09/809,889
CURRENT FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-809-889-32

Query Match 100.0%; Score 1547; DB 23; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.9e-159;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDAAISPAKDFLAGGVAIAISKTAVAPIERVKLLQVQHASKOITADKQKGIIDCVR 60
DB 1 MTDAAISPAKDFLAGGVAIAISKTAVAPIERVKLLQVQHASKOITADKQKGIIDCVR 60
QY 61 IPKQEVLSFMRGNLANIRYFPQALNFAFDKXKOIFLGVDKRTQFMRYPFAGNLASG 120
DB 61 IPKQEVLSFMRGNLANIRYFPQALNFAFDKXKOIFLGVDKRTQFMRYPFAGNLASG 120
QY 121 GAAGATSLCFYYPPLDFAFTRLAADVGAAGAREBERGGLDCLVKIKYSDGKGLYQGFNV 180
DB 121 GAAGATSLCFYYPPLDFAFTRLAADVGAAGAREBERGGLDCLVKIKYSDGKGLYQGFNV 180
QY 181 VGGIIRAAVFGIYDTAKGMLPDPKNTHTIVISWMIQVTAVALTSYFPDTRRRMM 240
DB 181 VGGIIRAAVFGIYDTAKGMLPDPKNTHTIVISWMIQVTAVALTSYFPDTRRRMM 240
QY 241 QSGRKGTDIMYTGTLDCWRKIARDEGGAFFKGAWSNVLKMGCAFVLVYDEIKK 298
DB 241 QSGRKGTDIMYTGTLDCWRKIARDEGGAFFKGAWSNVLKMGCAFVLVYDEIKK 298

RESULT 7

US-09-810-644-32
; Sequence 32, Application US/09810644
; GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.

APPLICANT: Pel, Yashong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
FILE REFERENCE: 660088.420D3
CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-810-644-32

Query Match 100.0%; Score 1547; DB 23; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.9e-159;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDALSPAKDPLAGVAAAISKTAAPIERVKLLQVHASKQITADKQYGIIDCVVR 60
DB 1 MTDALSPAKDPLAGVAAAISKTAAPIERVKLLQVHASKQITADKQYGIIDCVVR 60
QY 61 IPKEQEVLSFMRGNLANVIRYPTQALNFAFKDKKQIFLGVDKRTQFMRYFAGNLASG 120
DB 61 IPKEQEVLSFMRGNLANVIRYPTQALNFAFKDKKQIFLGVDKRTQFMRYFAGNLASG 120
QY 121 GAAGATSLCFYVPLDFATRLAADVGKAGAREFRGLDCLVKYKSGIKGLYOGFNVS 180
DB 121 GAAGATSLCFYVPLDFATRLAADVGKAGAREFRGLDCLVKYKSGIKGLYOGFNVS 180
QY 181 VOGIIYYAAVFGIYDTAKGMLPDPKNTIIVISWMIAGTVAVAGLTSYPPDYVRRMM 240
DB 181 VOGIIYYAAVFGIYDTAKGMLPDPKNTIIVISWMIAGTVAVAGLTSYPPDYVRRMM 240
QY 241 QSGRGTDMYTGTLDCWRKIARDGSGKAFKAGMSNVLRMGAFVLVLYDEIKKYT 298
DB 241 QSGRGTDMYTGTLDCWRKIARDGSGKAFKAGMSNVLRMGAFVLVLYDEIKKYT 298

RESULT 8
US-09-811-094-32.

Sequence 32, Application US/09811094
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wile, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pel, Yashong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
FILE REFERENCE: 660088.420D4
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-811-094-32

Query Match 100.0%; Score 1547; DB 23; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.9e-159;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDALSPAKDPLAGVAAAISKTAAPIERVKLLQVHASKQITADKQYGIIDCVVR 60
DB 1 MTDALSPAKDPLAGVAAAISKTAAPIERVKLLQVHASKQITADKQYGIIDCVVR 60

QY 61 IPKEQEVLSFMRGNLANVIRYPTQALNFAFKDKKQIFLGVDKRTQFMRYFAGNLASG 120
DB 61 IPKEQEVLSFMRGNLANVIRYPTQALNFAFKDKKQIFLGVDKRTQFMRYFAGNLASG 120
QY 121 GAAGATSLCFYVPLDFATRLAADVGKAGAREFRGLDCLVKYKSGIKGLYOGFNVS 180
DB 121 GAAGATSLCFYVPLDFATRLAADVGKAGAREFRGLDCLVKYKSGIKGLYOGFNVS 180
QY 181 VOGIIYYAAVFGIYDTAKGMLPDPKNTIIVISWMIAGTVAVAGLTSYPPDYVRRMM 240
DB 181 VOGIIYYAAVFGIYDTAKGMLPDPKNTIIVISWMIAGTVAVAGLTSYPPDYVRRMM 240
QY 241 QSGRGTDMYTGTLDCWRKIARDGSGKAFKAGMSNVLRMGAFVLVLYDEIKKYT 298
DB 241 QSGRGTDMYTGTLDCWRKIARDGSGKAFKAGMSNVLRMGAFVLVLYDEIKKYT 298

RESULT 9
US-09-811-132-32

Sequence 32, Application US/09811132
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wile, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pel, Yashong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
FILE REFERENCE: 660088.420D5
CURRENT APPLICATION NUMBER: US/09/811,132
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-811-132-32

Query Match 100.0%; Score 1547; DB 23; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.9e-159;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDALSPAKDPLAGVAAAISKTAAPIERVKLLQVHASKQITADKQYGIIDCVVR 60
DB 1 MTDALSPAKDPLAGVAAAISKTAAPIERVKLLQVHASKQITADKQYGIIDCVVR 60
QY 61 IPKEQEVLSFMRGNLANVIRYPTQALNFAFKDKKQIFLGVDKRTQFMRYFAGNLASG 120
DB 61 IPKEQEVLSFMRGNLANVIRYPTQALNFAFKDKKQIFLGVDKRTQFMRYFAGNLASG 120
QY 121 GAAGATSLCFYVPLDFATRLAADVGKAGAREFRGLDCLVKYKSGIKGLYOGFNVS 180
DB 121 GAAGATSLCFYVPLDFATRLAADVGKAGAREFRGLDCLVKYKSGIKGLYOGFNVS 180
QY 181 VOGIIYYAAVFGIYDTAKGMLPDPKNTIIVISWMIAGTVAVAGLTSYPPDYVRRMM 240
DB 181 VOGIIYYAAVFGIYDTAKGMLPDPKNTIIVISWMIAGTVAVAGLTSYPPDYVRRMM 240
QY 241 QSGRGTDMYTGTLDCWRKIARDGSGKAFKAGMSNVLRMGAFVLVLYDEIKKYT 298
DB 241 QSGRGTDMYTGTLDCWRKIARDGSGKAFKAGMSNVLRMGAFVLVLYDEIKKYT 298

RESULT 10
PCT-US02-01048-54
Sequence 54, Application PC/TUS0201048
GENERAL INFORMATION:
APPLICANT: EXLIXIS, INC.

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; TITLE OF INVENTION: Modulating Insulin Receptor Signaling
; FILE REFERENCE: EX02-001C-PC
; CURRENT APPLICATION NUMBER: PCT/US02/01048
; CURRENT FILING DATE: 2002-01-11
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-01048-54

Query Match          99.4%; Score 1537; DB 1; Length 298;
Best Local Similarity 99.3%; Pred. No. 3.5e-158;
Matches 296; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTDAAISPAKDFLAGVAAAIISKTAVAPIERVKLLQVOHASKQITADKQYKGIIDCVVR 60
Db 1 MTDAAVSPAKDFLAGVAAAIISKTAVAPIERVKLLQVOHASKQITADKQYKGIIDCVVR 60
Qy 61 IPKEQVLSFWRGNIANVIRYPTQALNPAFKDKYKQIFLGVDKRTQFWRYPAGNLSG 120
Db 61 IPKEQVLSFWRGNIANVIRYPTQALNPAFKDKYKQIFLGVDKRTQFWRYPAGNLSG 120
Qy 61 IPKEQVLSFWRGNIANVIRYPTQALNPAFKDKYKQIFLGVDKRTQFWRYPAGNLSG 120
Db 61 IPKEQVLSFWRGNIANVIRYPTQALNPAFKDKYKQIFLGVDKRTQFWRYPAGNLSG 120
Qy 121 GAAGATSLCFYVPLDPARTRIADAVGKAGAREFRGIDCLVKIYKSDGIKGLYQGFNV 180
Db 121 GAAGATSLCFYVPLDPARTRIADAVGKAGAREFRGIDCLVKIYKSDGIKGLYQGFNV 180
Qy 121 GAAGATSLCFYVPLDPARTRIADAVGKAGAREFRGIDCLVKIYKSDGIKGLYQGFNV 180
Db 121 GAAGATSLCFYVPLDPARTRIADAVGKAGAREFRGIDCLVKIYKSDGIKGLYQGFNV 180
Qy 181 VQGIITRAAYFGIYDPAKGLPDPKNTHTIVISWMIAGTVAAGLTSYPEDTVRRRMM 240
Db 181 VQGIITRAAYFGIYDPAKGLPDPKNTHTIVISWMIAGTVAAGLTSYPEDTVRRRMM 240
Qy 241 OSGRKGDIMYTGTLDCRKTIARDEGGAFFKGANSNVLKMGAFVLVYDEIKKYT 298
Db 241 OSGRKGDIMYTGTLDCRKTIARDEGGAFFKGANSNVLKMGAFVLVYDEIKKYT 298

RESULT 11
US-09-569-327-5
; Sequence 5, Application US/09569327
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clewenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Miller, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pel, Yashong
; APPLICANT: Carroll, Amy K.
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
; TITLE OF INVENTION: TRANSLATOR (ANT), NOVEL ANT LIGANDS
; TITLE OF INVENTION: AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.443
; CURRENT APPLICATION NUMBER: US/09/569.327
; CURRENT FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-569-327-5

Query Match          99.4%; Score 1537; DB 19; Length 298;
Best Local Similarity 99.3%; Pred. No. 3.5e-158;
Matches 296; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTDAAISPAKDFLAGVAAAIISKTAVAPIERVKLLQVOHASKQITADKQYKGIIDCVVR 60
Db 1 MTDAAVSPAKDFLAGVAAAIISKTAVAPIERVKLLQVOHASKQITADKQYKGIIDCVVR 60
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Qy 61 IPKEQVLSFWRGNIANVIRYPTQALNPAFKDKYKQIFLGVDKRTQFWRYPAGNLSG 120
Db 61 IPKEQVLSFWRGNIANVIRYPTQALNPAFKDKYKQIFLGVDKRTQFWRYPAGNLSG 120
Qy 121 GAAGATSLCFYVPLDPARTRIADAVGKAGAREFRGIDCLVKIYKSDGIKGLYQGFNV 180
Db 121 GAAGATSLCFYVPLDPARTRIADAVGKAGAREFRGIDCLVKIYKSDGIKGLYQGFNV 180
Qy 181 VQGIITRAAYFGIYDPAKGLPDPKNTHTIVISWMIAGTVAAGLTSYPEDTVRRRMM 240
Db 181 VQGIITRAAYFGIYDPAKGLPDPKNTHTIVISWMIAGTVAAGLTSYPEDTVRRRMM 240
Qy 241 OSGRKGDIMYTGTLDCRKTIARDEGGAFFKGANSNVLKMGAFVLVYDEIKKYT 298
Db 241 OSGRKGDIMYTGTLDCRKTIARDEGGAFFKGANSNVLKMGAFVLVYDEIKKYT 298

RESULT 12
US-10-466-162-54
; Sequence 54, Application US/10466162
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: Modulating Insulin Receptor Signaling
; FILE REFERENCE: EX02-001C-PC
; CURRENT APPLICATION NUMBER: US/10/466,162
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: US 60/261,335
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,694
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,532
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,361
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,531
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,457
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,226
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,304
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,459
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,456
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-466-162-54

Query Match          99.4%; Score 1537; DB 30; Length 298;
Best Local Similarity 99.3%; Pred. No. 3.5e-158;
Matches 296; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTDAAISPAKDFLAGVAAAIISKTAVAPIERVKLLQVOHASKQITADKQYKGIIDCVVR 60
Db 1 MTDAAVSPAKDFLAGVAAAIISKTAVAPIERVKLLQVOHASKQITADKQYKGIIDCVVR 60
Qy 61 IPKEQVLSFWRGNIANVIRYPTQALNPAFKDKYKQIFLGVDKRTQFWRYPAGNLSG 120
Db 61 IPKEQVLSFWRGNIANVIRYPTQALNPAFKDKYKQIFLGVDKRTQFWRYPAGNLSG 120
Qy 121 GAAGATSLCFYVPLDPARTRIADAVGKAGAREFRGIDCLVKIYKSDGIKGLYQGFNV 180
Db 121 GAAGATSLCFYVPLDPARTRIADAVGKAGAREFRGIDCLVKIYKSDGIKGLYQGFNV 180
Qy 181 VQGIITRAAYFGIYDPAKGLPDPKNTHTIVISWMIAGTVAAGLTSYPEDTVRRRMM 240
Db 181 VQGIITRAAYFGIYDPAKGLPDPKNTHTIVISWMIAGTVAAGLTSYPEDTVRRRMM 240
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Db 181 VGGIIIRAAVFGIYDTAKGMLPDPKNTHTIVISWMIAGTVTAAGTSPFPTVRRMM 240
241 QSGRKGTDIMYTGTLDCWKRKIADEGGKAFPGKAMSNVLRGMGAFLVLYDEIKKYT 298
Db 241 QSGRKGTDIMYTGTLDCWKRKIADEGGKAFPGKAMSNVLRGMGAFLVLYDEIKKYT 298

RESULT 13

US-60-452-680-20286
; Sequence 20286, Application US/60452680
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: GRUPE, Andrew
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01450
; CURRENT APPLICATION NUMBER: US/60/452,680
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20286
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-452-680-20286

Query Match 99.4%; Score 1537; DB 32; Length 298;
Best Local Similarity 99.3%; Pred. No. 3.5e-158;
Matches 296; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTDAAISPAKDFLAGGVAIAISKTAVAPIERVKLLQVQASKOITADKQYGIIDCVR 60
Db 1 MTDAAISPAKDFLAGGVAIAISKTAVAPIERVKLLQVQASKOITADKQYGIIDCVR 60
QY 61 IPKQGVLSFMRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKRTQPMRYFAGNLASG 120
Db 61 IPKQGVLSFMRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKRTQPMRYFAGNLASG 120
QY 121 GAAGATSLCFYVPLDPARTRLAADVGKAGAREFRGLDCLVKIYKSDIGIKLYOGFNVS 180
Db 121 GAAGATSLCFYVPLDPARTRLAADVGKAGAREFRGLDCLVKIYKSDIGIKLYOGFNVS 180
QY 181 VGGIIIRAAVFGIYDTAKGMLPDPKNTHTIVISWMIAGTVTAAGTSPFPTVRRMM 240
Db 181 VGGIIIRAAVFGIYDTAKGMLPDPKNTHTIVISWMIAGTVTAAGTSPFPTVRRMM 240
QY 241 QSGRKGTDIMYTGTLDCWKRKIADEGGKAFPGKAMSNVLRGMGAFLVLYDEIKKYT 298
Db 241 QSGRKGTDIMYTGTLDCWKRKIADEGGKAFPGKAMSNVLRGMGAFLVLYDEIKKYT 298

RESULT 14

US-09-760-469-1767
; Sequence 1767, Application US/09760469
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT254
; CURRENT APPLICATION NUMBER: US/09/760,469
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1983
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1767
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE

QY 1 MTDAAISPAKDFLAGGVAIAISKTAVAPIERVKLLQVQASKOITADKQYGIIDCVR 60
Db 1 MTDAAISPAKDFLAGGVAIAISKTAVAPIERVKLLQVQASKOITADKQYGIIDCVR 60
QY 61 IPKQGVLSFMRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKRTQPMRYFAGNLASG 120
Db 61 IPKQGVLSFMRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKRTQPMRYFAGNLASG 120
QY 121 GAAGATSLCFYVPLDPARTRLAADVGKAGAREFRGLDCLVKIYKSDIGIKLYOGFNVS 180
Db 121 GAAGATSLCFYVPLDPARTRLAADVGKAGAREFRGLDCLVKIYKSDIGIKLYOGFNVS 180
QY 181 VGGIIIRAAVFGIYDTAKGMLPDPKNTHTIVISWMIAGTVTAAGTSPFPTVRRMM 240
Db 181 VGGIIIRAAVFGIYDTAKGMLPDPKNTHTIVISWMIAGTVTAAGTSPFPTVRRMM 240
QY 241 QSGRKGTDIMYTGTLDCWKRKIADEGGKAFPGKAMSNVLRGMGAFLVLYDEIKKYT 298
Db 241 QSGRKGTDIMYTGTLDCWKRKIADEGGKAFPGKAMSNVLRGMGAFLVLYDEIKKYT 298

; LOCATION: (11)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-760-469-1767

Query Match 99.4%; Score 1537; DB 22; Length 332;
Best Local Similarity 99.3%; Pred. No. 4.1e-158;
Matches 296; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTDAAISPAKDFLAGGVAIAISKTAVAPIERVKLLQVQASKOITADKQYGIIDCVR 60
Db 35 MTDAAISPAKDFLAGGVAIAISKTAVAPIERVKLLQVQASKOITADKQYGIIDCVR 94
QY 61 IPKQGVLSFMRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKRTQPMRYFAGNLASG 120
Db 95 IPKQGVLSFMRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKRTQPMRYFAGNLASG 154
QY 121 GAAGATSLCFYVPLDPARTRLAADVGKAGAREFRGLDCLVKIYKSDIGIKLYOGFNVS 180
Db 155 GAAGATSLCFYVPLDPARTRLAADVGKAGAREFRGLDCLVKIYKSDIGIKLYOGFNVS 214
QY 181 VGGIIIRAAVFGIYDTAKGMLPDPKNTHTIVISWMIAGTVTAAGTSPFPTVRRMM 240
Db 215 VGGIIIRAAVFGIYDTAKGMLPDPKNTHTIVISWMIAGTVTAAGTSPFPTVRRMM 274
QY 241 QSGRKGTDIMYTGTLDCWKRKIADEGGKAFPGKAMSNVLRGMGAFLVLYDEIKKYT 298
Db 275 QSGRKGTDIMYTGTLDCWKRKIADEGGKAFPGKAMSNVLRGMGAFLVLYDEIKKYT 332

RESULT 15

US-10-216-583-1767
; Sequence 1767, Application US/10216583
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT254C1N
; CURRENT APPLICATION NUMBER: US/10/216,583
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/760,469
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1983
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1767
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (8)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: misc_feature
; LOCATION: (11)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

QY 1 MTDAAISPAKDFLAGGVAIAISKTAVAPIERVKLLQVQASKOITADKQYGIIDCVR 60
Db 35 MTDAAISPAKDFLAGGVAIAISKTAVAPIERVKLLQVQASKOITADKQYGIIDCVR 94
QY 61 IPKQGVLSFMRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKRTQPMRYFAGNLASG 120
Db 95 IPKQGVLSFMRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKRTQPMRYFAGNLASG 154
QY 121 GAAGATSLCFYVPLDPARTRLAADVGKAGAREFRGLDCLVKIYKSDIGIKLYOGFNVS 180
Db 155 GAAGATSLCFYVPLDPARTRLAADVGKAGAREFRGLDCLVKIYKSDIGIKLYOGFNVS 214
QY 181 VGGIIIRAAVFGIYDTAKGMLPDPKNTHTIVISWMIAGTVTAAGTSPFPTVRRMM 240
Db 215 VGGIIIRAAVFGIYDTAKGMLPDPKNTHTIVISWMIAGTVTAAGTSPFPTVRRMM 274
QY 241 QSGRKGTDIMYTGTLDCWKRKIADEGGKAFPGKAMSNVLRGMGAFLVLYDEIKKYT 298
Db 275 QSGRKGTDIMYTGTLDCWKRKIADEGGKAFPGKAMSNVLRGMGAFLVLYDEIKKYT 332

US-10-216-583-1767

Query Match 99.4%; Score 1537; DB 28; Length 332;
 Best Local Similarity 99.3%; Pred. No. 4.1e-158;
 Matches 296; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MTDAALSFADFLAGVAAAI	SKTAVAPIERVKLLLOVQHAS	KOITADKOYKGIIDCV	60
Db	35	MTDAAVSFADFLAGVAAAI	SKTAVAPIERVKLLLOVQHAS	KOITADKOYKGIIDCV	94
Qy	61	IPKEQVLSFWRGNLANVIR	YFPTQALNFAFKDKYKQI	FLGGVDKRTQFWRYFAGN	120
Db	95	IPKEQVLSFWRGNLANVIR	YFPTQALNFAFKDKYKQI	FLGGVDKRTQFWRYFAGN	154
Qy	121	GAAGATSLCFVYPLDFA	RTLAADVGRGAERERGLG	DCLVKTKSDGIKGLYQ	180
Db	155	GAAGATSLCFVYPLDFA	RTLAADVGRGAERERGLG	DCLVKTKSDGIKGLYQ	214
Qy	181	VOGIIYRAAVFGIYDTAK	GMLPDPKNTHTIVISMMIA	QVTAVAGLTSYPEDTVR	240
Db	215	VOGIIYRAAVFGIYDTAK	GMLPDPKNTHTIVISMMIA	QVTAVAGLTSYPEDTVR	274
Qy	241	QSGRKGTDIMYTGTLDC	WKRIARDEGGKAFPKGAM	SNVLRMGGAFTLVLYDE	298
Db	275	QSGRKGTDIMYTGTLDC	WKRIARDEGGKAFPKGAM	SNVLRMGGAFTLVLYDE	332

Search completed: December 18, 2003, 12:53:25
 Job time : 166.852 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:37:46 ; Search time 14.3494 Seconds
(without alignments)
1997.178 Million cell updates/sec

Title: US-09-811-131-32

Sequence: 1 MTDAALSPAKDFLAGVAA.....LRGKGAFVLVYDEIKYT 298

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:*

1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1547	100.0	298	1 A29132	ADP,ATP carrier pr
2	1479	95.6	298	2 S31814	ADP,ATP carrier pr
3	1458	94.2	298	2 B43646	ADP,ATP carrier pr
4	1454	94.0	298	1 S03894	ADP,ATP carrier pr
5	1419	91.7	298	1 XWBO	ADP,ATP carrier pr
6	1417	91.6	298	2 S37210	ADP,ATP carrier pr
7	1413	91.6	298	2 160173	adenine nucleotide
8	1413	91.3	298	1 A44778	ADP,ATP carrier pr
9	1170	75.6	300	1 S31935	ADP,ATP carrier pr
10	1032	66.7	300	2 T25371	hypothetical prote
11	1029	66.5	313	2 T23207	hypothetical prote
12	1029	66.5	313	2 T25850	hypothetical prote
13	986	63.7	300	2 T15206	ADP,ATP carrier pr
14	968	62.6	339	2 A41677	ADP,ATP carrier pr
15	938	60.6	301	2 S51132	ADP,ATP carrier pr
16	771	49.8	386	2 T09709	ADP,ATP carrier pr
17	770	49.8	386	2 T40526	adp/atp translocas
18	765	49.5	308	1 S30259	ADP,ATP carrier pr
19	761.5	49.1	307	2 A36582	ADP,ATP carrier pr
20	759	49.1	326	2 T25728	hypothetical prote
21	759	49.1	387	2 S14876	ADP,ATP carrier pr
22	757	48.9	313	1 XWNC	ADP,ATP carrier pr
23	754	48.7	386	2 S17917	ADP,ATP carrier pr
24	753	48.7	387	2 S15668	ADP,ATP carrier pr
25	752.5	48.6	318	1 A31978	ADP,ATP carrier pr
26	752	48.6	386	2 S21974	ADP,ATP carrier pr
27	749.5	48.4	305	2 S68154	ADP,ATP carrier pr
28	749.5	48.4	306	2 T20012	hypothetical prote
29	746	48.2	306	2 T42011	ADP,ATP carrier pr

30	746	48.2	379	2 T04608	ADP,ATP carrier pr
31	745.5	48.2	385	1 S29852	ADP,ATP carrier pr
32	745	48.2	382	2 S33630	ADP,ATP carrier pr
33	741.5	47.9	379	2 S21313	ADP,ATP carrier pr
34	741.5	47.9	386	2 S14874	ADP,ATP carrier pr
35	728	47.1	309	2 A24849	ADP,ATP carrier pr
36	665.5	43.0	298	2 T24029	hypothetical prote
37	521.5	33.7	327	2 T51577	ADP/ATP translocas
38	388	25.1	325	2 T04273	hypothetical prote
39	372	24.0	381	2 T51158	hypothetical prote
40	372	24.0	415	2 T48171	hypothetical prote
41	356	23.0	352	2 T01729	mitochondrial solu
42	350	22.6	475	2 T50686	peroxisomal Ca-dep
43	340	22.0	358	2 T45934	hypothetical prote
44	334	21.6	348	2 D84798	probable mitochon
45	322.5	20.8	332	2 T47703	Ca-dependent solut

ALIGNMENTS

RESULT 1

A29132
ADP,ATP carrier protein T2 - human

N:Alternate names: mitochondrial ADP,ATP translocase 2

C:Species: Homo sapiens (man)

C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000

C:Accession: A29132; C28116

R:Battini, R.; Ferrarini, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baegega, R.

J. Biol. Chem. 262, 4355-4359, 1987

A:Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulat

A:Reference number: A29132; MUID:87166056; PMID:3031073

A:Accession: A29132

A:Molecule type: mRNA

A:Residues: 1-298 <BAT>

A:Cross-references: GB:J02683; NID:G179246; PIDN:AAA35579.1; PID:G179247

R:Holmdorff, J.; Attardi, G.

Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988

A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a

A:Reference number: A94197; MUID:88124845; PMID:2829183

A:Accession: C28116

A:Molecule type: mRNA

A:Residues: 47-65, 'G', 67-110, 'L', 112-161, 'G', 163-298 <HOU>

A:Cross-references: GB:J03551; NID:G339720; PIDN:AAA36749.1; PID:G339721

A:Experimental source: Clone pBAT3

C:Genetics:

A:Gene: GDB:AMT2; T3; 2P1

A:Cross-references: GDB:125190; OMIM:300150

A:Map position: Xq13-Xq26

A>Note: There may be some confusion in the assignment of sequences for GDB:AMT2 and GDB:

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C:Keywords: duplication; homodimer; mitochondrial; transmembrane protein

F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACB1>

F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACB2>

F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACB3>

Query Match	100.0%	Score 1547	DB 1	Length 298
Best Local Similarity	100.0%	Pred. No. 4e-130		
Matches 298	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MTDAALSPAKDFLAGVAA	ISKTNVAPIERVKLLIQVHASKQITADKOYKGIIDCVNR	60
DB	1	MTDAALSPAKDFLAGVAA	ISKTNVAPIERVKLLIQVHASKQITADKOYKGIIDCVNR	60
QY	61	IPKQEVLSFPRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFMWYFAGNLASG		120
DB	61	IPKQEVLSFPRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFMWYFAGNLASG		120
QY	121	GAAGATSLCFYVPLDPAFTRIAADVAGKGAERFERGLDCLVTKYSGDIGKLVOGFVNS		180
DB	121	GAAGATSLCFYVPLDPAFTRIAADVAGKGAERFERGLDCLVTKYSGDIGKLVOGFVNS		180
QY	181	VOGIIITPAALFGLYDRAKGLPDPKXTHIVISMNIAGQTVAVAGLTSYPPDYARRRMM		240

Db 181 VGGIITVAAAFGIYDTAKGMLPDPKNTHTIVISWIAQTVAVAGLTSPPTVARRMM 240
 Qy 241 QSGRGKTDIMYTGTLDCWRKIARDGSKAFKFGAMSNVLRGMGAFVLYVDEIKK 298
 Db 241 QSGRGKTDIMYTGTLDCWRKIARDGSKAFKFGAMSNVLRGMGAFVLYVDEIKK 298

RESULT 2

ADP, ATP carrier protein T2 - mouse
 N:Alternate names: adenine nucleotide translocase
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Apr-1998
 C:Accession: S31814
 R:Coates, P.; Laplace, C.
 submitted to the EMBL Data Library, January 1993
 A:Reference number: S31814
 A:Accession: S31814
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-298 <COS>
 A:Cross-references: EMBL:X70847
 C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
 C:Keywords: duplication; transmembrane protein
 F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP>
 F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 95.6%; Score 1479; DB 2; Length 298;
 Best Local Similarity 95.6%; Pred. No. 4, 5e-124;
 Matches 285; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MTDAAISPAKDFLAGVAAAIKTAVAPIERKLLQVQHASKQITADKQYKGIIDCYR 60
 Db 1 MTDAAISPAKDFLAGVAAAIKTAVAPIERKLLQVQHASKQITADKQYKGIIDCYR 60
 Qy 61 IPKEQEVLSFMRGNLANVIRYFPTQALNFAFKDKTKQIFLGVDKRTQFMRFAAGNLASG 120
 Db 61 IPKEQGVLSFMRGNLANVIRYFPTQALNFAFKDKTKQIFLGVDKRTQFMRFAAGNLASG 120
 Qy 121 GAAGTSLCFVYPLDPAFTRILADVGKAGAREPFGLDCLVKYKSGIKGLYGGFNVS 180
 Db 121 GAAGTSLCFVYPLDPAFTRILADVGKAGAREPFGLDCLVKYKSGIKGLYGGFNVS 180
 Qy 181 VGGIITVAAAFGIYDTAKGMLPDPKNTHTIVISWIAQTVAVAGLTSPPTVARRMM 240
 Db 181 VGGIITVAAAFGIYDTAKGMLPDPKNTHTIVISWIAQTVAVAGLTSPPTVARRMM 240
 Qy 241 QSGRGKTDIMYTGTLDCWRKIARDGSKAFKFGAMSNVLRGMGAFVLYVDEIKK 298
 Db 241 QSGRGKTDIMYTGTLDCWRKIARDGSKAFKFGAMSNVLRGMGAFVLYVDEIKK 298

RESULT 3

ADP, ATP carrier protein T2 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999
 C:Accession: B43646
 R:Powell, S.J.; Wedd, S.M.; Runswick, M.J.; Walker, J.E.
 Biochemistry 28, 866-873, 1989
 A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
 A:Reference number: B43646; MUID:89229093; PMID:2540808
 A:Accession: B43646
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-298 <POM>
 A:Cross-references: GB:M24103; NID:9529416; PIDN:AAA30769.1; PID:9529417
 C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP>

F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 94.2%; Score 1458; DB 2; Length 298;
 Best Local Similarity 92.9%; Pred. No. 3, 4e-122;
 Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MTDAAISPAKDFLAGVAAAIKTAVAPIERKLLQVQHASKQITADKQYKGIIDCYR 60
 Db 1 MTDAAISPAKDFLAGVAAAIKTAVAPIERKLLQVQHASKQITADKQYKGIIDCYR 60
 Qy 61 IPKEQEVLSFMRGNLANVIRYFPTQALNFAFKDKTKQIFLGVDKRTQFMRFAAGNLASG 120
 Db 61 IPKEQGVLSFMRGNLANVIRYFPTQALNFAFKDKTKQIFLGVDKRTQFMRFAAGNLASG 120
 Qy 121 GAAGTSLCFVYPLDPAFTRILADVGKAGAREPFGLDCLVKYKSGIKGLYGGFNVS 180
 Db 121 GAAGTSLCFVYPLDPAFTRILADVGKAGAREPFGLDCLVKYKSGIKGLYGGFNVS 180
 Qy 181 VGGIITVAAAFGIYDTAKGMLPDPKNTHTIVISWIAQTVAVAGLTSPPTVARRMM 240
 Db 181 VGGIITVAAAFGIYDTAKGMLPDPKNTHTIVISWIAQTVAVAGLTSPPTVARRMM 240
 Qy 241 QSGRGKTDIMYTGTLDCWRKIARDGSKAFKFGAMSNVLRGMGAFVLYVDEIKK 296
 Db 241 QSGRGKTDIMYTGTLDCWRKIARDGSKAFKFGAMSNVLRGMGAFVLYVDEIKK 296

RESULT 4

ADP, ATP carrier protein T3 - human
 S03894

N:Alternate names: ADP, ATP carrier protein T2 (misidentification); mitochondrial ADP, ATP
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
 C:Accession: S03894; B28116
 J:Cozens, A.L.; Runswick, M.J.; Walker, J.E.
 J. Mol. Biol. 206, 261-280, 1989

A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr
 A:Reference number: S03893; MUID:89236396; PMID:2541251
 A:Accession: S03894

A:Status: not compared with conceptual translation
 A:Molecule type: DNA

A:Residues: 1-298 <COS>
 R:Holdsworth, J.; Attardi, G.
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
 A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a

A:Reference number: A94197; MUID:88124845; PMID:2829183
 A:Accession: B28116

A:Molecule type: mRNA
 A:Residues: 36-104, 'R', 106, 'A', 109-298 <HOU>

A:Cross-references: GB:J03592; NID:9339722; PIDN:AAA36750.1; PID:9339723

A:Experimental source: liver
 C:Genetics:

A:Gene: GDB:ANT3; ANT3X
 A:Cross-references: GDB:125184; OMIM:300151; OMIM:403000

A:Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
 A:Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and GDB:
 C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:2-298/Product: ADP, ATP carrier protein #status_predicted <MNT>
 F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 94.0%; Score 1454; DB 1; Length 298;
 Best Local Similarity 92.6%; Pred. No. 7, 6e-122;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MTDAAISPAKDFLAGVAAAIKTAVAPIERKLLQVQHASKQITADKQYKGIIDCYR 60
 Db 1 MTDAAISPAKDFLAGVAAAIKTAVAPIERKLLQVQHASKQITADKQYKGIIDCYR 60
 Qy 61 IPKEQEVLSFMRGNLANVIRYFPTQALNFAFKDKTKQIFLGVDKRTQFMRFAAGNLASG 120
 Db 61 IPKEQGVLSFMRGNLANVIRYFPTQALNFAFKDKTKQIFLGVDKRTQFMRFAAGNLASG 120

Db 61 IPKEQVLSFWRGMLANVIRYPTQALNFAEKDYKKQIFLGVDKHTQFMRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDPARTRLAADVGKAGBERBGLGDCIVTKYKSGITGLYQGFVNS 180
 Db 121 GAAGATSLCFVYPLDPARTRLAADVGKAGBERBGLGDCIVTKYKSGITGLYQGFVNS 180
 QY 181 VGGIIIRAAVFGIYDPAKGLPDPKNTHTIVSMIAQVTAVAGLTSYPEDTVRRMM 240
 Db 181 VGGIIIRAAVFGIYDPAKGLPDPKNTHTIVSMIAQVTAVAGLTSYPEDTVRRMM 240
 QY 241 QSGRKGTDIMYTGTLDCWKRIADDEGKAPFKGAMSVNLKMGGAFLVLYDEIKK 296
 Db 241 QSGRKGADIMYTGTLDCWKRIADDEGKAPFKGAMSVNLKMGGAFLVLYDEIKK 296

RESULT 5

WBO
 ADP, ATP carrier protein T1 - bovine
 N/Alternate names: ADP/ATP translocase T1
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 14-Nov-1993 #sequence_revision 22-Jul-1994 #text_change 22-Jun-1999
 C/Accession: A43646; A24822; A03181; A61343; S69369
 R/Powell, S.J.; Medd, S.M.; Rumsick, M.J.; Walker, J.R.
 Biochemistry 28, 866-873, 1989
 A/Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
 A/Reference number: A43646; MUID:89229093; PMID:2540808
 A/Accession: A43646
 A/Molecule type: mRNA
 A/Residues: 1-298 <POM>
 A/Cross-references: GB:M24102; NID:9529414; PIDN:AAA30768.1; PID:9529415
 R/Rasmussen, U.B.; Mohlirab, H.
 Biochem. Biophys. Res. Commun. 138, 850-857, 1986
 A/Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unusual
 A/Reference number: A24822; MUID:86295775; PMID:3017341
 A/Accession: A24822
 A/Molecule type: mRNA
 A/Residues: 208-298 <RAS>
 A/Cross-references: GB:M13783; NID:9162630; PIDN:AAA30363.1; PID:9162631
 R/Aquila, H.; Mista, D.; Bullitz, M.; Klingenberg, M.
 Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982
 A/Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondrion
 A/Reference number: A03181; MUID:82188267; PMID:7076130
 A/Accession: A03181
 A/Molecule type: protein
 A/Residues: 2-51, 'X', 53-70, 'X', 72-109, 'X', 111-298 <AGU>
 A/Note: residue 52 may be methyllysine
 R/Babel, W.; Wachter, E.; Aquila, H.; Klingenberg, M.
 Biochim. Biophys. Acta 670, 176-180, 1981
 A/Title: Amino acid sequence determination of the ADP/ATP carrier from beef heart mitoch
 A/Reference number: A61343; MUID:82046808; PMID:6271240
 A/Accession: A61343
 A/Molecule type: protein
 A/Residues: 205-298 <BAB>
 R/Oetmeier, W.; Masson, K.; Kalina, S.
 Eur. J. Biochem. 227, 730-733, 1995
 A/Title: [(3)H]-7-azido-4-isopropylisocitidone labels Cys159 of the bovine mitochondrial ADP
 A/Reference number: S69369; MUID:95172058; PMID:7867632
 A/Accession: S69369
 A/Molecule type: protein
 A/Residues: 49-63, 154-168 <OET>
 C/Comment: This protein is synthesized in the cytosol and transported into the mitochondrion
 C/Complex: homodimer
 C/Function:
 A/Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP genera
 A/Note: located in the inner mitochondrial membrane
 C/Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
 C/Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mitoch
 F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>
 F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
 F:52/Modified site: N6-methyllysine (Lys) #status predicted

Query Match 91.6%; Score 1419; DB 1; Length 298;
 Best Local Similarity 89.9%; Pred. No. 1e-118;
 Matches 267; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTDAAISFADPLAGVAAAISKTAVPIERVKLLQVHASKQITADKQYKGIIDCVVR 60
 Db 1 MSDQALSFLDPLAGVAAAISKTAVPIERVKLLQVHASKQISAKQYKGIIDCVVR 60
 QY 61 IPKEQVLSFWRGMLANVIRYPTQALNFAEKDYKKQIFLGVDKHTQFMRYFAGNLASG 120
 Db 61 IPKEQVLSFWRGMLANVIRYPTQALNFAEKDYKKQIFLGVDKHTQFMRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDPARTRLAADVGKAGBERBGLGDCIVTKYKSGITGLYQGFVNS 180
 Db 121 GAAGATSLCFVYPLDPARTRLAADVGKAGBERBGLGDCIVTKYKSGITGLYQGFVNS 180
 QY 181 VGGIIIRAAVFGIYDPAKGLPDPKNTHTIVSMIAQVTAVAGLTSYPEDTVRRMM 240
 Db 181 VGGIIIRAAVFGIYDPAKGLPDPKNTHTIVSMIAQVTAVAGLTSYPEDTVRRMM 240
 QY 241 QSGRKGTDIMYTGTLDCWKRIADDEGKAPFKGAMSVNLKMGGAFLVLYDEIKK 297
 Db 241 QSGRKGADIMYTGTLDCWKRIADDEGKAPFKGAMSVNLKMGGAFLVLYDEIKK 297

RESULT 6

S37210
 ADP, ATP carrier protein T1 - mouse
 N/Alternate names: adenine nucleotide carrier
 C/Species: Mus musculus (house mouse)
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
 C/Accession: S37210
 R/Laplace, C.; Costet, P.
 submitted to the EMBL Data Library, September 1993
 A/Reference number: S37210
 A/Accession: S37210
 A/Molecule type: preliminary
 A/Status: preliminary
 A/Residues: 1-298 <LAP>
 A/Cross-references: EMBL:X74510; NID:9402627; PIDN:CAA52616.1; PID:9402628
 C/Genetics:
 A/Gene: ANCL
 C/Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
 C/Keywords: duplication; transmembrane protein
 F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 91.6%; Score 1417; DB 2; Length 298;
 Best Local Similarity 89.6%; Pred. No. 1.5e-118;
 Matches 266; Conservative 15; Mismatches 16; Indels 0; Gaps 0;
 QY 1 MTDAAISFADPLAGVAAAISKTAVPIERVKLLQVHASKQITADKQYKGIIDCVVR 60
 Db 1 MGDQALSFLDPLAGVAAAISKTAVPIERVKLLQVHASKQISAKQYKGIIDCVVR 60
 QY 61 IPKEQVLSFWRGMLANVIRYPTQALNFAEKDYKKQIFLGVDKHTQFMRYFAGNLASG 120
 Db 61 IPKEQVLSFWRGMLANVIRYPTQALNFAEKDYKKQIFLGVDKHTQFMRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDPARTRLAADVGKAGBERBGLGDCIVTKYKSGITGLYQGFVNS 180
 Db 121 GAAGATSLCFVYPLDPARTRLAADVGKAGBERBGLGDCIVTKYKSGITGLYQGFVNS 180
 QY 181 VGGIIIRAAVFGIYDPAKGLPDPKNTHTIVSMIAQVTAVAGLTSYPEDTVRRMM 240
 Db 181 VGGIIIRAAVFGIYDPAKGLPDPKNTHTIVSMIAQVTAVAGLTSYPEDTVRRMM 240
 QY 241 QSGRKGTDIMYTGTLDCWKRIADDEGKAPFKGAMSVNLKMGGAFLVLYDEIKK 297
 Db 241 QSGRKGADIMYTGTLDCWKRIADDEGKAPFKGAMSVNLKMGGAFLVLYDEIKK 297

RESULT 7

160173

adenine nucleotide translocator - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999

C:Accession: 160173

R:Shinohara, Y.; Kamida, M.; Yamazaki, N.; Terada, H.

B:Biochim. Biophys. Acta 1152, 192-196, 1993

A:Title: Isolation and characterization of cDNA clones and a genomic clone encoding rat

A:Reference number: 160173; MUID:94002161; PMID:8399300

A:Accession: 160173

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-298 <RES>

A:Cross-references: EMBL:X61667; NID:5400426; PIDN:CAA43842.1; PID:5400427

C:Genetics:

A:Gene: anti

A:Introns: 37/3; 200/1; 247/1

C:Superfamily: ADP,ATP carrier protein, ADP,ATP carrier protein repeat homology

C:Keywords: duplication; transmembrane protein

F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match

Beat Local Similarity 91.6%; Score 1417; DB 2; Length 298;

Matches 266; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

```
QY 1 MTDAALSPAKDFLAGVAAATSKTAVAPIERVKLLQVQHSKQJTDADKQYKGIIDCVRR 60
DB 1 MGDHALSPKDFLAGVAAATSKTAVAPIERVKLLQVQHSKQJTDADKQYKGIIDCVRR 60
QY 61 IPKEQEVLSFMRGNLANVIRYFPQALNFAFDKTKQKIFLGVDKRTQFMRYPAGNLASG 120
DB 61 IPKEGGLSFMRGNLANVIRYFPQALNFAFDKTKQKIFLGVDKRTQFMRYPAGNLASG 120
QY 121 GAAGATSTCFYYPDLPATRLAADVKGAKAREPFGDGLVTKYKSDGIGLYGFVNS 180
DB 121 GAAGATSTCFYYPDLPATRLAADVKGAKAREPFGDGLVTKYKSDGIGLYGFVNS 180
QY 121 GAAGATSTCFYYPDLPATRLAADVKGAKAREPFGDGLVTKYKSDGIGLYGFVNS 180
DB 121 GAAGATSTCFYYPDLPATRLAADVKGAKAREPFGDGLVTKYKSDGIGLYGFVNS 180
QY 181 VGGIIYAAAFYGYDITKAGMLPDPKNTHTIVSNMIAQTVAVAGLTSYPPDTPVRRMM 240
DB 181 VGGIIYAAAFYGYDITKAGMLPDPKNTHTIVSNMIAQTVAVAGLTSYPPDTPVRRMM 240
QY 181 VGGIIYAAAFYGYDITKAGMLPDPKNTHTIVSNMIAQTVAVAGLTSYPPDTPVRRMM 240
DB 181 VGGIIYAAAFYGYDITKAGMLPDPKNTHTIVSNMIAQTVAVAGLTSYPPDTPVRRMM 240
QY 241 QSGRGKTDIMYTGTLDCWRKIARDEGGAFFKGAWSNVLKGMGAFVLVLYDEIKKY 297
DB 241 QSGRGKTDIMYTGTLDCWRKIARDEGGAFFKGAWSNVLKGMGAFVLVLYDEIKKY 297
```

RESULT 8

A44778

ADP,ATP carrier protein T1 - human

N:Alternate names: mitochondrial ADP,ATP translocase 1

C:Species: Homo sapiens (man)

C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000

C:Accession: A44778; S03893; A39891; A28116

R:Li, K.; Warner, C.K.; Hodges, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, M.

J: Biol. Chem. 264, 13998-14004, 1989

A:Title: A human muscle adenine nucleotide translocator gene has four exons, is located

A:Reference number: A44778; MUID:89340499; PMID:2547778

A:Accession: A44778

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-298 <LIA>

A:Cross-references: GB:J04982; NID:5178658; PIDN:AAA51736.1; PID:5178659

R:Cozen, A.L.; Kunswick, M.J.; Walker, J.E.

J: Mol. Biol. 206, 261-280, 1989

A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr

A:Accession: S03893

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-298 <COZ>

R:Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.

Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987

A:Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader

A:Reference number: A39891; MUID:88041149; PMID:2823266

A:Accession: A39891

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-15, 'A', 17-146, 'RR', 149, 151-226, 'L', 228-298 <NEC>

A:Cross-references: GB:J02966; NID:5339919; PIDN:AAA61233.1; PID:5339920

A:Experimental source: clone pRNAAT

R:Houldsworth, J.; Attard, G.

Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988

A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a

A:Reference number: A9197; MUID:88124845; PMID:2829183

A:Accession: A28116

A:Molecule type: mRNA

A:Residues: 1-37 <HOV>

A:Cross-references: GB:J03593; NID:5339724; PIDN:AAA6751.1; PID:5339725

A:Experimental source: liver

C:Genetics:

A:Gene: GDB:ANT1; T1

A:Cross-references: GDB:119680; OMIM:103220

A:Map position: 4q35-4q35

C:Superfamily: ADP,ATP carrier protein, ADP,ATP carrier protein repeat homology

C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein

F:2-298/Product: ADP,ATP carrier protein status predicted <MAT>

F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match

Beat Local Similarity 91.3%; Score 1413; DB 1; Length 298;

Matches 265; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

```
QY 1 MTDAALSPAKDFLAGVAAATSKTAVAPIERVKLLQVQHSKQJTDADKQYKGIIDCVRR 60
DB 1 MGDHALSPKDFLAGVAAATSKTAVAPIERVKLLQVQHSKQJTDADKQYKGIIDCVRR 60
QY 61 IPKEQEVLSFMRGNLANVIRYFPQALNFAFDKTKQKIFLGVDKRTQFMRYPAGNLASG 120
DB 61 IPKEGGLSFMRGNLANVIRYFPQALNFAFDKTKQKIFLGVDKRTQFMRYPAGNLASG 120
QY 121 GAAGATSTCFYYPDLPATRLAADVKGAKAREPFGDGLVTKYKSDGIGLYGFVNS 180
DB 121 GAAGATSTCFYYPDLPATRLAADVKGAKAREPFGDGLVTKYKSDGIGLYGFVNS 180
QY 121 GAAGATSTCFYYPDLPATRLAADVKGAKAREPFGDGLVTKYKSDGIGLYGFVNS 180
DB 121 GAAGATSTCFYYPDLPATRLAADVKGAKAREPFGDGLVTKYKSDGIGLYGFVNS 180
QY 181 VGGIIYAAAFYGYDITKAGMLPDPKNTHTIVSNMIAQTVAVAGLTSYPPDTPVRRMM 240
DB 181 VGGIIYAAAFYGYDITKAGMLPDPKNTHTIVSNMIAQTVAVAGLTSYPPDTPVRRMM 240
QY 181 VGGIIYAAAFYGYDITKAGMLPDPKNTHTIVSNMIAQTVAVAGLTSYPPDTPVRRMM 240
DB 181 VGGIIYAAAFYGYDITKAGMLPDPKNTHTIVSNMIAQTVAVAGLTSYPPDTPVRRMM 240
QY 241 QSGRGKTDIMYTGTLDCWRKIARDEGGAFFKGAWSNVLKGMGAFVLVLYDEIKKY 297
DB 241 QSGRGKTDIMYTGTLDCWRKIARDEGGAFFKGAWSNVLKGMGAFVLVLYDEIKKY 297
```

RESULT 9

S31935

ADP,ATP carrier protein - African malaria mosquito

C:Species: Anopheles gambiae (African malaria mosquito)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S31935; S31936

R:Beard, C.B.; Crews-Oyen, A.E.; Collins, F.H.

submitted to the EMBL Data Library, February 1993

A:Description: A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae.

A:Reference number: S31935

A:Accession: S31935

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-301 <BEA>

A:Cross-references: EMBL:Z21814; EMBL:Z21815

C:Superfamily: ADP,ATP carrier protein, ADP,ATP carrier protein repeat homology

C:Keywords: duplication; transmembrane protein

F:7-101/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F;112-204/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;209-300/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match	75.6%;	Score 1170;	DB 1;	Length 301;
Best Local Similarity	78.1%;	Pred. No. 1.5e-96;		
Matches 225;	Conservative 18;	Mismatches 45;	Indels 0;	Gaps 0

Qy 8 FADPFLAGVAAAIKSTAAPIERVELLQVQHAKEQITADKQYGGIIDDVLRPEKEQEV 67

Db 10 FADPFLAGGISAIVKSTAAPIERVELLQVQHAKEQITADKQYGGIIDDVLRPEKEQI 69

Qy 68 LSTRKGLNANVIRYPTQALNFAFKDKYQITLGGVDKRTQPMRYEAGNTLASGGAAGATS 127

Db 70 GAFQGGNLNANVIRYPTQALNFAFKDKYQVQLGGVDKRTQPMRYEAGNTLASGGAAGATS 129

Qy 128 LCFEYVPLDFAFRTLRADVCGAKAGAREFRGLGCLVKIKYSDQIKELVGGFNVSVQGGIIY 167

Db 130 LCFYVPLDFAFRTLRADVCGAGERRFRNGLLDCLKRYKSDGIIELIRGFNVSVQGGIIY 169

Qy 188 RAAVFGIYDTAKGMLDPKNTNTHIVISWMLAQCTVTVAGLTSPDPDYRRMMQSGKGT 247

Db 190 RAAVFGCFDTAKGMLDPPKNTSIFVSWMLAQVTVTASGIIISPEFDYVRRMMQSNPKCS 249

Qy 248 DIATYGLDQWRKIALDEGGKAPFGKAMNNTLRMGKAPVTVLDEIK 295

Db 250 EIVTKNTLDCWVKLIGQKSGAEPFKAPFNNVLRGGQALVLFVDEYK 297

RESULT 10
T25371

hypothetical protein T27E9.1 - *Caenorhabditis elegans*

C:species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C:Accession: T25371

Query Match	Score	DB 2	Length	300
66.7%	1032			

	Matches	203;	Conservative	34;	Mismatches	50;	Indels	4;	Gaps	3
Qy	8	FAKQFLAGVAAAI	SKTAVAP	IERVYKLL	LIQV	QASKQTAD	KQYGIID	CVTRIP	REGEV	67
Db	12	FLIDLASG	GTAAAY	SKTAVAP	IERVYKLL	LIQV	QDASKA	LAVD	RKYGIID	VLIRVEQGV
Qy	68	LSFWRGNL	ANVIRY	PTQALN	FAFDK	YKQI	PLG	GVDR	KTOPFWR	YFAGNLASGGAAGATS
Db	72	AALWRGNL	ANVIRY	PTQALN	FAFD	YKQI	PLG	GVDR	KTOPFWR	YFAGNLASGGAAGATS
Qy	128	LCFVYPLD	PARTR	LAADV	GKAGAE	RRFKGL	GDCL	VYKYS	DSGI	KGLYQGFNV
Db	132	LCFVYPLD	PARTR	LAADV	GKAGAE	RRFKGL	GDCL	VYKYS	DSGI	KGLYQGFNV
Qy	188	RAA	VEG	IVDT	AKGML	-	PD	PK	TH	YISNM
Db	191	RAA	VEG	IVDT	AKGML	-	PD	PK	TH	YISNM
Qy	247	TDIM	ATG	GLD	CRK	KL	AR	B	E	G
Db	250	DIL	K	N	L	D	CRK	KL	AR	B

RESULT 11
T23207

hypothetical protein K01H12.2 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C:Accession: T23207

Query Match	66.5%;	Score 1029;	DB 2;	length 313;
Best Local Similarity	70.8%;	Pred. No. 5.6e-84;		
Matches 206;	Conservative 28;	Mismatches 53;	Indels 4;	Gaps 3;

QY 8 FADFDLAGVAAAIKSTAAPIERKYLLOVQVHASKOLTDKQYKGIIDCVLRPEQEV 67

QY 25 FLIDLDSGGTAANAESTAAPIERKYLLOVQVDSLTITADKRRKGIIDVULVVRKEQGY 84

QY 68 LSFWRGNLANVIRYPTQALNFAFDKYKQIPLGQVDRKTFQWRYFAGNLASGGAGATS 127

Db 85 AALMRGNLANVIRYPTQALNFAFDKYKNIPOGLDKKDDFMKRFAGNLASGGAGATS 144

QY 128 LCFVRYPLDFAFTRLADYQKAGABEPRGLDPCVYKISKDGIKGLQGFNVSVQGIITV 187

Db 145 LCFVRYPLDFAFTRLADYQKAGABEPRGLDPCVYKISKDGIKGLQGFNVSVQGIITV 203

QY 188 RAAVFGIYDTAKGM-LPDPKNTHTVISMIAQVTAAGLTSYDPDTRRRMMQSGRG 246

Db 204 RAAVFGMFDTAAMVFAFDGKLNFPFAAIAIQVTVVSGIITSYPMPTVRRMMQSGRK- 262

QY 247 TDIMTYGTLDCWRKTLARQEGKAPFKGAMSVULAGMGAPVULVYDSIKKX 297

Db 263 -DVLVKNYTLDCAVKTIKNKGSAVMEKGLSNVFGTGGALVLAITYDSIQRF 312

RESULT 12

hypothetical protein T01B1.4 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C:Accession: T25850

Query Match	66.5%	Score 1029;	DB 2;	Length 313;
Best Local Similarity	70.8%	Pred. No. 5.6e-84;		
Matches 206;	Conservative 28;	Mismatches 53;	Indels 4;	Gaps 3;


```

Db      63 RVSKEQVLSLRGNVANVIRYFPTQAFNFAKDYFNIF-PRYDQNTDFSKFCVNILS 121
QY      120 GGAAGATSLCFYYPIDPAFTRIAADVKGAGAREERGLDCLVLYKSDGIKGLYQGFNV 179
Db      122 GATGAGATSLILVYPIDPAFTRIASDIGN-KDROFTGLPDCLAKLYKQGLSLYSFGGV 180
QY      180 SVQGIITIRAAVFGIYDTAKGML-PDPKATHIVISMIAGVTAVAGLTSYFPDTRRRM 238
Db      181 SVTGIIVRGSYFGIYDSKALLFTNDKNTNIVLKNVAQSVTIIAGLISYFPDTRRRM 240
QY      239 MMQSGRKG-TDIMYTGTLDCWRKLIARDEGKAFPGGANSNVLKMGGAFLVLVLYDEIKK 296
Db      241 MMMSGRKGEKBIQYKNTIDCWIKILRNBSGFKGFPKGAMNANVIRGAGALVLVLYDELOK 299

```

Search completed: December 18, 2003, 12:44:04
 Job time : 14.3494 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OW protein - protein search, using sw model

Run on: December 18, 2003, 12:36:16 / Search time 8.34267 Seconds
(without alignments)
1679.794 Million cell updates/sec

Title: US-09-811-131-32

Perfect score: 1547
Sequence: 1 MTDALSPAKPLAGVAA.....LRGNGAFVLYLDEIKKYT 298

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1537	99.4	298	1	ADT2_HUMAN
2	1525	98.6	298	1	ADT2_RAT
3	1519	98.2	298	1	ADT2_MOUSE
4	1458	94.2	298	1	ADT3_BOVIN
5	1454	94.0	298	1	ADT3_HUMAN
6	1417	91.6	298	1	ADT1_MOUSE
7	1414	91.4	297	1	ADT1_BOVIN
8	1413	91.3	298	1	ADT1_HUMAN
9	1253.5	81.0	299	1	ADT_DROME
10	1190	76.9	301	1	ADT_ANOGA
11	968	62.6	339	1	ADT_CHUKE
12	771	49.8	386	1	ADT1_GOSHI
13	770	49.8	322	1	ADT_SCHPO
14	765	49.5	308	1	ADT_CHIRE
15	761.5	49.2	307	1	ADT3_YEAST
16	759	49.1	387	1	ADT1_MAIZE
17	757	48.9	313	1	ADT_NEUCR
18	753.5	48.7	385	1	ADT2_ARATH
19	753	48.7	387	1	ADT2_MAIZE
20	752.5	48.6	318	1	ADT2_YEAST
21	752	48.6	386	1	ADT1_SOLTU
22	750	48.5	382	1	ADT_ORYSA
23	749.5	48.4	305	1	ADT_KLULA
24	747.5	48.3	381	1	ADT1_ARATH
25	744	48.1	331	1	ADT1_WHEAT
26	741.5	47.9	386	1	ADT2_SOLTU
27	737	47.6	331	1	ADT2_WHEAT
28	737	47.1	309	1	ADT1_YEAST
29	728	47.1	309	1	ADT1_YEAST
30	312.5	20.2	565	1	CMC2_CABEL
31	307	19.8	588	1	CMC2_CABEL
32	285	18.4	330	1	GDC_BOVIN
33	284	18.4	307	1	ODC2_YEAST

34	278	18.0	325	1	UCP5_MOUSE
35	276.5	17.9	322	1	GDC_RAT
36	276.5	17.9	702	1	CMC1_CABEL
37	276	17.8	678	1	CMC1_HUMAN
38	274	17.7	325	1	UCP5_HUMAN
39	265.5	17.2	332	1	GDC_HUMAN
40	265	17.1	306	1	CMG5_MOUSE
41	261.5	16.9	675	1	CMC2_HUMAN
42	261	16.9	310	1	ODC1_YEAST
43	257.5	16.6	315	1	MPT_HUMAN
44	256	16.5	303	1	CM69_HUMAN
45	249.5	16.1	326	1	YEO8_SCHPO

ALIGNMENTS

RESULT 1
ADT2_HUMAN STANDARD, PRT, 298 AA.
AC P05141, O43350;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLIC25A5 OR ANT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Primates; Carnivora; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=90375457; PubMed=2168878;
RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Wurzel J.;
RT "The human fibroblast adenine nucleotide translocator gene. Molecular
cloning and sequence.";
RT J. Biol. Chem. 265:16060-16063 (1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=8716056; PubMed=3031073;
RA Battini R., Ferrari S., Kaczmarek L., Calabretta B., Chen S.T.,
RT Baerger R.;
RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
growth-regulated.";
RT J. Biol. Chem. 262:4355-4358 (1987).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen C.N., Su Y., Baydayan P., Siruno A., Nagaraja R.,
RA Mazarella R.A., Schlesinger D., Chen E.Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Becker M., Graves T., Ozersky P.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 47-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houldsworth J., Attardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
level in adult human liver.";
RT Proc. Natl. Acad. Sci. U.S.A. 85:377-381 (1988).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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 CC or send an email to license@isb-sib.ch).

DR EMBL; M57424; AAA51737.1; -
 DR EMBL; J02683; AAA55579.1; -
 DR EMBL; L78810; AAB39266.1; -
 DR EMBL; AC004000; AAB96347.1; -
 DR EMBL; J03591; AAB36749.1; -
 DR F1R; A29132; A29132.
 DR Genew; HGNC:10991; SLC25A5.
 DR MIM; 300150; -
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.
 DR GO; GO:0015207; P: adenine transporter activity; TAS.
 DR GO; GO:0006832; P: small molecule transport; TAS.
 DR InterPro; IPR002067; Mtc_carrier.
 DR InterPro; IPR002030; Mtc_uncoupling.
 DR Pfam; PF00153; mltc_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 FT CONFLICT 6 6 V -> L (IN REF. 2).
 FT CONFLICT 66 66 G -> E (IN REF. 2).
 FT CONFLICT 111 111 R -> L (IN REF. 4 AND 5).
 FT CONFLICT 162 162 V -> G (IN REF. 5).
 SQ SEQUENCE 298 AA; 32895 MW; F973C3AED92C49D3 CRC64;

Query Match 99.4%; Score 1537; DB 1; Length 298;
 Best Local Similarity 99.3%; Pred. No. 8,9e-128;
 Matches 296; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

QY 1 MTDALSPAKDPLAGVAAAIKTAAPRIERVKLLQVHASKQITADKQYGIIDCVRR 60
 DB 1 MTDAAVSFAKDFLAGVAAAIKTAAPRIERVKLLQVHASKQITADKQYGIIDCVRR 60
 QY 61 IPKEQEVLSFMRGNLANVIRYPTQALNFAFDKTKQIFLGVDKRTQFMRYPAGNLASG 120
 DB 61 IPKEQGVLSFMRGNLANVIRYPTQALNFAFDKTKQIFLGVDKRTQFMRYPAGNLASG 120
 QY 121 GAAGATSLCFYPLDFAFRLAADVGKAGAREFRGLDCLVKYKSGIKLYGPFNV 180
 DB 121 GAAGATSLCFYPLDFAFRLAADVGKAGAREFRGLDCLVKYKSGIKLYGPFNV 180
 QY 181 VGGIITRAAYFGIYDTAKGMLPDPKNTHTIVISWMLAQTVAVAGLTSPPTVRRMM 240
 DB 181 VGGIITRAAYFGIYDTAKGMLPDPKNTHTIVISWMLAQTVAVAGLTSPPTVRRMM 240
 QY 241 QSGRGKTDIMYGTLDCKWKIARDEGKAFKFGKANSVLRGGAFLVLYDEIKK 298
 DB 241 QSGRGKTDIMYGTLDCKWKIARDEGKAFKFGKANSVLRGGAFLVLYDEIKK 298

RESULT 2
 ADT2 RAT STANDARD; PRT; 298 AA.
 AC 009073;
 DT 01-FEB-1995 (rel. 31, Created)
 DT 01-FEB-1995 (rel. 31, Last sequence update)

DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
 CC (Adenine nucleotide translocator 2) (ANT 2).
 GN SLC25A5 OR ANT2.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=94002161; PubMed=8399300;
 RA Shinozaki Y., Kanada M., Yamazaki N., Terada H.;
 RT "Isolation and characterization of cDNA clones and a genomic clone
 RT encoding rat mitochondrial adenine nucleotide translocator."
 RL Biochim. Biophys. Acta 1152:192-196(1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND
 CC SKELETAL MUSCLE.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).

DR EMBL; D12771; BAA02338.1; -
 DR InterPro; IPR002067; Mtc_carrier.
 DR InterPro; IPR002030; Mtc_uncoupling.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mltc_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32901 MW; 6A59204B987E9E35 CRC64;

Query Match 98.6%; Score 1525; DB 1; Length 298;
 Best Local Similarity 98.3%; Pred. No. 1e-126;
 Matches 293; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTDALSPAKDPLAGVAAAIKTAAPRIERVKLLQVHASKQITADKQYGIIDCVRR 60
 DB 1 MTDAAVSFAKDFLAGVAAAIKTAAPRIERVKLLQVHASKQITADKQYGIIDCVRR 60
 QY 61 IPKEQEVLSFMRGNLANVIRYPTQALNFAFDKTKQIFLGVDKRTQFMRYPAGNLASG 120
 DB 61 IPKEQGVLSFMRGNLANVIRYPTQALNFAFDKTKQIFLGVDKRTQFMRYPAGNLASG 120
 QY 121 GAAGATSLCFYPLDFAFRLAADVGKAGAREFRGLDCLVKYKSGIKLYGPFNV 180
 DB 121 GAAGATSLCFYPLDFAFRLAADVGKAGAREFRGLDCLVKYKSGIKLYGPFNV 180
 QY 181 VGGIITRAAYFGIYDTAKGMLPDPKNTHTIVISWMLAQTVAVAGLTSPPTVRRMM 240
 DB 181 VGGIITRAAYFGIYDTAKGMLPDPKNTHTIVISWMLAQTVAVAGLTSPPTVRRMM 240

DB 181 VGGIIYRAAFYGLYDTAKGLPDPKXTHIFISWMIASQVTAVALGTSYPPDVTVRMM 240

QY 241 OSGRKTDIMTGTLDCKRKIARDGSGKAFKGAWSNLRGMGAFVLYLDEIKKTT 238

DB 241 OSGRKTDIMTGTLDCKRKIARDGSGKAFKGAWSNLRGMGAFVLYLDEIKKTT 238

RESULT 3

ID ADT2_MOUSE STANDARD; PRT; 298 AA.

AC P51881; Q61311;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DB ADP, ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)

DB (Adenine nucleotide translocator 2) (ANT 2).

GN SLC25A5 OR ANT2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Brain;

RX MEDLINE=97059403; PubMed=8903724;

RA Ellison J.W., Li X., Francke U., Shapiro L.J.,

RT "Rapid evolution of human pseudautosomal genes and their mouse homologs."

RL Mamm. Genome 7:25-30(1996).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Skeletal muscle;

RA Sheldon J.G.,

RL Thesis (1995), University of Cambridge, U.K.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=129/Sv;

RA Cochet P., Laplace C.,

RT Submitted (FEB-1993) to the EMBL/Genbank/DBJ databases.

RN [4]

RP REVISIONS.

RA Laplace C.,

RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.

RN [5]

RP SEQUENCE FROM N.A.

RX MEDLINE=20432087; PubMed=10974536;

RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.,

RT "Expression and sequence analysis of the mouse adenine nucleotide translocase 1 and 2 genes."

RL Gene 254:57-66(2000).

CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.

CC -1- SUBUNIT: Homodimer.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.

CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

CC -----

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CC -----

CC EMBL: U27316; AAC52838.1; -

CC EMBL: U10404; AA19009.1; -

CC EMBL: X70847; CA50196.1; -

CC EMBL: AF240003; AAF64471.1; -

CC MGI: MGI:1353496; SLC25A5.

CC InterPro: IPR002067; Mlt_carrier.

CC InterPro: IPR002030; Mlt_uncoupling.

DR InterPro: IPR001993; Mitoch_carrier.

DR Pfam: PF00153; mito_carr; 3

DR PRINTS: PRO0926; MITOCARRIER.

DR PRINTS: PRO0784; MTUNCOUPLING.

DR PROSITE: PS00215; MITOCH_CARRIER; 3.

KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport; Multi-gene family.

KW Multi-gene family.

FT TRANSMEM 12 29 1 (POTENTIAL).

FT TRANSMEM 73 91 2 (POTENTIAL).

FT TRANSMEM 117 134 3 (POTENTIAL).

FT TRANSMEM 176 195 4 (POTENTIAL).

FT TRANSMEM 214 231 5 (POTENTIAL).

FT TRANSMEM 273 291 6 (POTENTIAL).

FT REPEAT 1 111 1.

FT REPEAT 112 208 2.

FT REPEAT 209 298 3.

SO SEQUENCE 298 AA; 32931 MW; 0798B04B987E8E20 CRC64;

Query Match 98.2%; Score 1519; DB 1; Length 298;

Best Local Similarity 98.0%; Pred. No. 3.4e-126;

Matches 292; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTDAAISPAKDFLAGVAAAIKTAVALPIERVKLLQVQHASKOITADKOYKGIIDCVVR 60

DB 1 MTDAAISPAKDFLAGVAAAIKTAVALPIERVKLLQVQHASKOITADKOYKGIIDCVVR 60

QY 61 IPKEQVLSFMRGLANVIRFPQALNPAFKDKYKQIFLGVDKRTQFWRYPAGNTLASG 120

DB 61 IPKEQVLSFMRGLANVIRFPQALNPAFKDKYKQIFLGVDKRTQFWRYPAGNTLASG 120

QY 121 GAAGATSLCFYPPDPATRLAADVKGARBERFGIDCLVLYKSGDIGLQGFNV 180

DB 121 GAAGATSLCFYPPDPATRLAADVKGARBERFGIDCLVLYKSGDIGLQGFNV 180

QY 121 VGGIIYRAAFYGLYDTAKGLPDPKXTHIFISWMIASQVTAVALGTSYPPDVTVRMM 240

DB 181 VGGIIYRAAFYGLYDTAKGLPDPKXTHIFISWMIASQVTAVALGTSYPPDVTVRMM 240

QY 241 OSGRKTDIMTGTLDCKRKIARDGSGKAFKGAWSNLRGMGAFVLYLDEIKKTT 238

DB 241 OSGRKTDIMTGTLDCKRKIARDGSGKAFKGAWSNLRGMGAFVLYLDEIKKTT 238

RESULT 4

ID ADT3_BOVIN STANDARD; PRT; 298 AA.

AC P32007;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DB ADP, ATP carrier protein, isoform T2 (ADP/ATP translocase 3) (Adenine nucleotide translocator 3) (ANT 3).

GN SLC25A6 OR ANT3.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89228993; PubMed=2540808;

RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.,

RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed differences in various tissues."

RL Biochemistry 28:866-873(1989).

CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.

CC -1- SUBUNIT: Homodimer.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.

CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

CC -----

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EMBL; M24103; AAA30769.1; -
 DR PIR; B43646; B43646.
 DR InterPro; IPR002067; Mit carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_car.3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUOCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 2 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 129 298 3.
 SQ SEQUENCE 298 AA; 32877 MW; 1C34E7DF6EDE4061 CRC64;

Query Match 94.2%; Score 1458; DB 1; Length 298;
 Beel Local Similarity 92.9%; Pred. No. 7.7e-121;
 Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 MTDALSPAKDPLAGVAIAIKTAAPAPERVKLLQVQVHAKQVOTADKQVGIIDCVR 60
 DB 1 MTEQAIISPKDPLAGVAIAIKTAAPAPERVKLLQVQVHAKQVOTADKQVGIIDCVR 60
 QY 61 IPKEQEVLSFWKGNLANVIRYPTQALNFAFDKTKQIPLGVDKRTQFWRYFAQNLASG 120
 DB 61 IPKEQGVLSFWKGNLANVIRYPTQALNFAFDKTKQIPLGVDKRTQFWRYFAQNLASG 120
 QY 121 GAAGATSTCFVYPLDPARTRLADYVKGAKAEFFGLDCLVYIKYSQDGIKLYGQFNVS 180
 DB 121 GAAGATSTCFVYPLDPARTRLADYVKGAKAEFFGLDCLVYIKYSQDGIKLYGQFNVS 180
 QY 181 VGGIIYBAAYGIDYTKAGMLPDPKNTHTVSNMIAQVTAAGLTSYPTVRRMM 240
 DB 181 VGGIIYBAAYGIDYTKAGMLPDPKNTHTVSNMIAQVTAAGLTSYPTVRRMM 240
 QY 241 QSGRGKTDIMYTGTLDCWRKIKARDEGKAFKAGANSVLRGNGAFVLYLVDIIRK 296
 DB 241 QSGRGKTDIMYTGTLDCWRKIKARDEGKAFKAGANSVLRGNGAFVLYLVDIIRK 296

RESULT 5
 ADT3 HUMAN STANDARD; PRT; 298 AA.
 ID ADT3_HUMAN
 AC P12336; O96C49;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE ADP/ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3)
 GN (Adenine nucleotide translocator 3) (ANT 3).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89236396; PubMed=2541251;
 RA Cozens A.L., Runswick M.J., Walker J.E.;

"DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP translocase." J. Mol. Biol. 206:261-280 (1989).

RP SEQUENCE FROM N.A.
 RA Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A., Margolin J.F.,
 RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

RP TISSUE=Brain, Cervix, Eye, and Lung;
 RX MEDLINE=22389257; PubMed=12477932;

RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner U., Shemen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uedlin T.B., Toshitsuki S., Carrinck P., Prange C., Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Pahay J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmitt J., Myers R.M., Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RP SEQUENCE OF 36-298 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=88124845; PubMed=2829183;

RA Houldsworth J., Actardi G.,
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in adult human liver." Proc. Natl. Acad. Sci. U.S.A. 85:377-381 (1988).

CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.

CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

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CC EMBL; J03592; AAA36750.1; -
 CC EMBL; AY007135; AAG01998.1; -
 CC EMBL; BC007295; AAH07295.1; -
 CC EMBL; BC007850; AAH07850.1; -
 CC EMBL; BC008737; AAH08737.1; -
 CC EMBL; BC008935; AAH08935.1; -
 CC EMBL; BC014775; AAH14775.1; -
 CC PIR; S03894; S03894.
 CC Gene; HGNC:10992; SLC25A6.
 CC MIM; 300151; -
 CC MIM; 403000; -
 CC GO; GO:0005744; C:mitochondrial inner membrane translocase co. .; TAS.
 CC GO; GO:0005471; F:ATP/ADP antiporter activity; TAS.
 CC GO; GO:0006854; P:ATP/ADP exchange; TAS.
 CC InterPro; IPR002067; Mit carrier.
 CC InterPro; IPR002030; Mit_uncoupling.
 CC InterPro; IPR001993; Mitoch_carrier.

DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 MW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 100 1.
 FT REPEAT 101 208 2.
 FT REPEAT 209 298 3.
 FT REPEAT 105 108 4.
 FT CONFLICT 242 242 S -> F (IN REF. 3; AAHL1475).
 FT SEQUENCE 298 AA; 32866 MW; 1853489F0B49672P CRC64;
 Query Match 94.0%; Score 1454; DB 1; Length 298;
 Best Local Similarity 92.6%; Pred. No. 1.7e-120;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MTDAAISPAKDFLAGGVAASIKTAAPVIERVKLLQVQHASKQITDQKGIIDCVR 60
 1 MTEQAIISPAKDFLAGGVAASIKTAAPVIERVKLLQVQHASKQITDQKGIIDCVR 60
 DB 1 IPKQGVLSFWRGNLANVIRFPYQALNPAKDKKKQIFLGVDVKRTFPRNFRANL 120
 61 IPKQGVLSFWRGNLANVIRFPYQALNPAKDKKKQIFLGVDVKRTFPRNFRANL 120
 DB 1 IPKQGVLSFWRGNLANVIRFPYQALNPAKDKKKQIFLGVDVKRTFPRNFRANL 120
 61 IPKQGVLSFWRGNLANVIRFPYQALNPAKDKKKQIFLGVDVKRTFPRNFRANL 120
 QY 121 GAAGATSLCFYVPLDPAFTRIAADVGKAGRRBPGGLDCLYKIKSGDIGLVQGFV 180
 121 GAAGATSLCFYVPLDPAFTRIAADVGKAGRRBPGGLDCLYKIKSGDIGLVQGFV 180
 DB 121 GAAGATSLCFYVPLDPAFTRIAADVGKAGRRBPGGLDCLYKIKSGDIGLVQGFV 180
 121 GAAGATSLCFYVPLDPAFTRIAADVGKAGRRBPGGLDCLYKIKSGDIGLVQGFV 180
 QY 181 VQGIIVYAAFGYIDTAKGMLPDKNTHIVISWMLAQTVAAVAGLTSYPPDYRRMM 240
 181 VQGIIVYAAFGYIDTAKGMLPDKNTHIVISWMLAQTVAAVAGLTSYPPDYRRMM 240
 DB 181 VQGIIVYAAFGYIDTAKGMLPDKNTHIVISWMLAQTVAAVAGLTSYPPDYRRMM 240
 181 VQGIIVYAAFGYIDTAKGMLPDKNTHIVISWMLAQTVAAVAGLTSYPPDYRRMM 240
 QY 241 QSGRRKADIMYTGVDWCWKIFRDEGKAFKFGAANSVLRGGAFLVLYDELKK 296
 241 QSGRRKADIMYTGVDWCWKIFRDEGKAFKFGAANSVLRGGAFLVLYDELKK 296
 DB 241 QSGRRKADIMYTGVDWCWKIFRDEGKAFKFGAANSVLRGGAFLVLYDELKK 296
 241 QSGRRKADIMYTGVDWCWKIFRDEGKAFKFGAANSVLRGGAFLVLYDELKK 296

RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
 RT "Expression and sequence analysis of the mouse adenine nucleotide
 RT translocase 1 and 2 genes.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sheueman C.M., Schuller G.D.,
 RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin J., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Tohiyuki S., Carrinci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton B., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Binkley K.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1 FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1 SUBUNIT: Homodimer.
 CC -1 SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1 DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1 SIMILARITY: Belongs to the mitochondrial carrier family.
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL; U27315; AAC52837.1; -
 CC EMBL; X74510; CAAS2616.1; -
 CC EMBL; AF240002; AAF64470.1; -
 CC EMBL; BC003791; AAH03791.1; -
 CC EMBL; BC026925; AAH26925.1; -
 CC PIR; S37210; S37210.
 CC MGI; MGI:1353495; Slc25a4.
 DR InterPro; IPR002067; Mit carrier.
 DR InterPro; IPR002030; Mit uncoupling.
 DR InterPro; IPR001993; Mitoch carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 MW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 208 2.
 FT REPEAT 209 298 3.
 FT CONFLICT 136 136 F -> L (IN REF. 1).
 FT SEQUENCE 298 AA; 32904 MW; 3A849FEAB0981462 CRC64;
 Query Match 91.6%; Score 1417; DB 1; Length 298;

Best Local Similarity 89.6%, Pred. No. 3.1e-117, Matches 266; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 MTDAALSPAKDFLAGGVAALISKTAVAPIERVKLLQVQHASKQITADKQYGIIDCVRR 60
 DB 1 MGDAALSLKDFLAGGIAAASKTAVAPIERVKLLQVQHASKQISAEKQYGIIDCVRR 60
 QY 61 IPKEQEVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKRTQFWRFPAGNLASG 120
 DB 61 IPKEQGLFSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKRTQFWRFPAGNLASG 120
 QY 121 GAAGATSLCFYVPLDPFATRIADAVGKSGSQRERFNGLDCLTKIKPSGLKGLYQGFSSVS 180
 DB 121 GAAGATSLCFYVPLDPFATRIADAVGKSGSQRERFNGLDCLTKIKPSGLKGLYQGFSSVS 180
 QY 181 VGGIIITRAAYFGIYDTAKGMLPDPKNTHTIVISNMIAQTVAAGLTSYPPDTPVRRMM 240
 DB 181 VGGIIITRAAYFGIYDTAKGMLPDPKNTHTIVISNMIAQTVAAGLTSYPPDTPVRRMM 240
 QY 241 OSGRKGDIMYTGTLDCWRKIARDGKGAFFKGSANVLRGMAFVLVYDEIKKY 297
 DB 241 OSGRKGDIMYTGTLDCWRKIARDGKGAFFKGSANVLRGMAFVLVYDEIKKY 297

RESULT 7
 ADT1 RAT STANDARD; PRT; 298 AA.

AC Q05962;
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
 GN SLC25A4 OR ANT1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OK NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley, and Mistar; TISSUE=Heart, and Liver;
 RX MEDLINE=94002161; PubMed=8399300;
 RA Shinohara Y., Kanada M., Yamazaki N., Terada H.;
 RT "Isolation and characterization of cDNA clones and a genomic clone encoding rat mitochondrial adenine nucleotide translocator";
 RL Biochim. Biophys. Acta 1152:192-196(1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
 CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER EXTENT, IN BRAIN AND KIDNEY.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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 CC -----
 DR EMBL; X61667; CAA43842.1; -;
 DR EMBL; D12770; BAA02337.1; -;
 DR PIR; I60173; I60173.
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carr; 3-
 DR PRINTS; PRO0926; MITOCARRIER.
 DR PRINTS; PRO0784; MTOUNCOUPLING.

DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 3298 MM; 66704FF78C6BC320 CRC64;

Query Match 91.6%, Score 1417; DB 1; Length 298;
 Best Local Similarity 89.6%, Pred. No. 3.1e-117;
 Matches 266; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTDAALSPAKDFLAGGVAALISKTAVAPIERVKLLQVQHASKQITADKQYGIIDCVRR 60
 DB 1 MGDAALSLKDFLAGGIAAASKTAVAPIERVKLLQVQHASKQISAEKQYGIIDCVRR 60
 QY 61 IPKEQEVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKRTQFWRFPAGNLASG 120
 DB 61 IPKEQGLFSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKRTQFWRFPAGNLASG 120
 QY 121 GAAGATSLCFYVPLDPFATRIADAVGKSGSQRERFNGLDCLTKIKPSGLKGLYQGFSSVS 180
 DB 121 GAAGATSLCFYVPLDPFATRIADAVGKSGSQRERFNGLDCLTKIKPSGLKGLYQGFSSVS 180
 QY 181 VGGIIITRAAYFGIYDTAKGMLPDPKNTHTIVISNMIAQTVAAGLTSYPPDTPVRRMM 240
 DB 181 VGGIIITRAAYFGIYDTAKGMLPDPKNTHTIVISNMIAQTVAAGLTSYPPDTPVRRMM 240
 QY 241 OSGRKGDIMYTGTLDCWRKIARDGKGAFFKGSANVLRGMAFVLVYDEIKKY 297
 DB 241 OSGRKGDIMYTGTLDCWRKIARDGKGAFFKGSANVLRGMAFVLVYDEIKKY 297

RESULT 8
 ADT1 BOVIN STANDARD; PRT; 297 AA.

AC P02722;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP/ATP carrier protein, heart isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
 GN SLC25A4 OR ANT1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; Bovidae; Bovinae; Bos.
 OK NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=82188267; PubMed=2540808;
 RX POWELL S.J., MEDD S.M., RUNSWICK M.J., WALKER J.B.;
 RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed differences in various tissues";
 RL Biochemistry 28:866-873(1989).
 CC -----
 DR EMBL; M21882.1; M21882.1; -;
 DR EMBL; M21882.1; M21882.1; -;
 DR PIR; I60173; I60173.
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carr; 3-
 DR PRINTS; PRO0926; MITOCARRIER.
 DR PRINTS; PRO0784; MTOUNCOUPLING.

RT an unusually short 3'-noncoding sequence."

RL Biochem. Biophys. Res. Commun. 138:850-857(1986).

CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE

CC MITOCHONDRIAL INNER MEMBRANE.

CC -1- SUBUNIT: Homodimer.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial

CC inner membrane.

CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

CC -----

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CC or send an email to license@isb-sdb.ch).

CC -----

DR EMBL: M13783; AAA0363.1; -

DR EMBL: M24102; AAA0768.1; -

DR PIR: A43646; XMB0.

DR InterPro: IPR002067; Mt_carrier.

DR InterPro: IPR002030; Mt_uncoupling.

DR InterPro: IPR001993; Mitoch_carrier.

DR Pfam: PF00153; mito_carr; 3.

DR PRINTS: PR00926; MITOCARRIER.

DR PRINTS: PR00784; MTUNCARRIER.

DR PROSITE: PS00215; MITOCH_CARRIER; 3.

KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;

KW Multigene family; Methylation.

FT MOD RES 0 1 BLOCKED.

FT INIT MET 0 0

FT MOD RES 1 1 METHYLATION (POTENTIAL).

FT TRANS MEM 11 51 1 (POTENTIAL).

FT TRANS MEM 11 28 2 (POTENTIAL).

FT TRANS MEM 72 90 3 (POTENTIAL).

FT TRANS MEM 116 133 4 (POTENTIAL).

FT TRANS MEM 175 194 5 (POTENTIAL).

FT TRANS MEM 213 230 6 (POTENTIAL).

FT TRANS MEM 272 290 1 (POTENTIAL).

FT REPEAT 1 110 1.

FT REPEAT 111 207 2.

FT REPEAT 208 297 3.

SQ SEQUENCE 297 AA; 32836 MW; A582D3C4A40AEB48 CRC64;

Query Match 91.4%; Score 1414; DB 1; Length 297;

Best Local Similarity 89.9%; Pred. No. 5.6e-117;

Matches 266; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 2 TDAALSPADFLAGVAAAIKTAAPVPIERVLTALQVHASKQITADKQYGIIDCVRI 61

DB 1 SDQALSPKDFLAGVAAAIKTAAPVPIERVLTALQVHASKQITADKQYGIIDCVRI 60

QY 62 PKEQEVLSFWRGNLNVIRYPTQALNFAFDKQYQIFLGGVDKRTQFWRYPAGNLASGG 121

DB 61 PKEQEVLSFWRGNLNVIRYPTQALNFAFDKQYQIFLGGVDKRTQFWRYPAGNLASGG 120

QY 122 AAGATSLCFYVPLDPAFRTLADVKGAKAERFRGLGCLYKITYSDGIGKLYGFNSV 181

DB 121 AAGATSLCFYVPLDPAFRTLADVKGAKAERFRGLGCLYKITYSDGIGKLYGFNSV 180

QY 182 QGIIIRAYRAGIYDTAKGMLPDPNGTHIVISMMIAQVTVAVAGTSYPPPTVRRMMMO 241

DB 181 QGIIIRAYRAGIYDTAKGMLPDPNGTHIVISMMIAQVTVAVAGTSYPPPTVRRMMMO 240

QY 242 SGRKGTDMITGTLDQWRKIARDEGKAPFKGAWNSVLKMGCAFVLVLYDEIKKY 297

DB 241 SGRKGTDMITGTLDQWRKIARDEGKAPFKGAWNSVLKMGCAFVLVLYDEIKKY 296

RESULT 9

ADTI HUMAN STANDARD; PRT; 298 AA.

ID ADTI HUMAN

AC P12235;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP

DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1).

GN SLG2544 OR ANT1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OK NCBI_TaxId=9606;

RN [1]

RN SEQUENCE FROM N.A.

RP MEDLINE=89236396; PubMed=2541251;

RT Cozens A.L., Runswick M.J., Walker J.E.

RT "DNA sequences of two expressed nuclear genes for human mitochondrial

RT ADP/ATP translocase."

RL J. Mol. Biol. 206:261-280(1989).

RN [2]

RN SEQUENCE FROM N.A.

RP MEDLINE=89340499; PubMed=2547778;

RT Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,

RT Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;

RT "A human muscle adenine nucleotide translocator gene has four exons,

RT is located on chromosome 4, and is differentially expressed."

RL J. Biol. Chem. 264:13998-14004(1989).

RN [3]

RN SEQUENCE FROM N.A.

RP MEDLINE=88041149; PubMed=2823266;

RT Nekehlmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;

RT "cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack

RT of a leader peptide, divergence from a fibroblast translocator cDNA,

RT and coevolution with mitochondrial DNA genes."

RL Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).

RN [4]

RN SEQUENCE FROM N.A.

RP TISSUE=EYE;

RC MEDLINE=22388257; PubMed=12477932;

RT Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RT Klausner R.D., Collins P.S., Wagner L., Shemen C.M., Schuler G.D.,

RT Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bat N.K.,

RT Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RT Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RT Stadleiro M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RT Brownstein M.J., Uedlin T.B., Toshiyuki S., Carrinzi P., Prange C.,

RT Rana S.S., Lequellano N.A., Peters G.J., Adrison R.D., Mullany S.J.,

RT Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RT Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RT Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RT Abbey J., Helton B., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RT Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RT Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RT Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RT Butlerfield Y.S.N., Krzywinski M.I., Skalska J., Smalins D.E.,

RT Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [5]

RN SEQUENCE OF 1-37 FROM N.A.

RP TISSUE=LIVER;

RC MEDLINE=88124845; PubMed=2829183;

RT Houldsworth J., Atterdall G.;

RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA

RT level in adult human liver."

RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).

RN [6]

RN VARIANTS PRO-114 AND MET-289.

RP MEDLINE=20385067; PubMed=10926541;

RT Kaakonien J., Uuseliu J.K., Tiranli V., Kyttala A., Zeviani M.,

RT Comi G.P., Keranen J., Peltomen L., Suomalainen A.;

RT "Role of adenine nucleotide translocator 1 in mtDNA maintenance."

RL Science 289:782-785(2000).

CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE

CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- DISEASE: Defects in SLIC25A4 are a cause of autosomal dominant
 CC progressive external ophthalmoplegia with various mitochondrial
 CC DNA deletions (PEO). Patients with PEO have mitochondrial
 CC myopathy, progressive external ophthalmoplegia, and other
 CC abnormalities associated with multiple different deletions of
 CC mitochondrial DNA.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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 CC -----
 CC DR EMBL: J02966; AAA61223.1; -.
 CC DR EMBL: J03593; AAA6751.1; -.
 CC DR EMBL: J04982; AAA51736.1; -.
 CC DR EMBL: BC008664; AA008664.1; -.
 CC DR PIR: A44778; A44778.
 CC DR Genew: HGNC:10990; SLIC25A4.
 CC DR MIM: 103220; -.
 CC DR MIM: 157640; -.
 CC DR GO: GO:0005887; C: integral to plasma membrane; TAS.
 CC DR GO: GO:0005739; C: mitochondrion; TAS.
 CC DR GO: GO:0015207; P: adenine transporter activity; TAS.
 CC DR GO: GO:0006091; P: energy pathways; TAS.
 CC DR GO: GO:0000002; P: mitochondrial genome maintenance; TAS.
 CC DR GO: GO:0006833; P: small molecule transport; TAS.
 CC DR InterPro: IPR002067; Mtc_carrier.
 CC DR InterPro: IPR002030; Mtc_uncoupling.
 CC DR InterPro: IPR001993; Mito_carrier.
 CC DR Pfam: PF00153; mto_car; 3.
 CC DR PRINTS: PR00926; MITOCARRIER.
 CC DR PRINTS: PR00784; MTUNCOUPLING.
 CC DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 CC DR Mitochondrion: Inner membrane; Repeat; Transmembrane; Transport;
 CC KM Multigene family; Disease mutation.
 CC FT TRANSMEM 12 29 1 (POTENTIAL).
 CC FT TRANSMEM 73 91 2 (POTENTIAL).
 CC FT TRANSMEM 117 134 3 (POTENTIAL).
 CC FT TRANSMEM 176 195 4 (POTENTIAL).
 CC FT TRANSMEM 214 231 5 (POTENTIAL).
 CC FT TRANSMEM 273 291 6 (POTENTIAL).
 CC FT REPEAT 1 110 1.
 CC FT REPEAT 111 208 2.
 CC FT REPEAT 209 298 3.
 CC FT VARIANT 114 114 A -> P (IN PEO).
 CC FT VARIANT 289 289 V -> M (IN PEO).
 CC FT VARIANT 289 289 /FTID=VAR_012111.
 CC FT CONFLICT 16 16 G -> A (IN REF. 3).
 CC FT CONFLICT 147 149 KGA -> R (IN REF. 3).
 CC FT CONFLICT 227 227 V -> L (IN REF. 3).
 CC SQ SEQUENCE .298 AA; 33064 MW; 59F0DDAECAE7FEBB CRC64;
 CC
 CC Query Match 91.3%; Score 1413; DB 1; Length 298;
 CC Best Local Similarity 89.2%; Pred. No. 6.9e-117;
 CC Matches 265; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 121 GAAGATSLCFYYPIDFARTRLAADVAGAGABERFGLDCLVKIKYSDGINGLYGFFNV 180
 DB 121 GAAGATSLCFYYPIDFARTRLAADVAGAGABERFGLDCLVKIKYSDGINGLYGFFNV 180
 QY 161 VGGIITVYAAAFPGIYDTAKGMLPPPKNTHIYISMMIACTVYAVGLTSYPPDTARRMM 240
 DB 161 VGGIITVYAAAFPGIYDTAKGMLPPPKNTHIYISMMIACTVYAVGLTSYPPDTARRMM 240
 QY 241 OSGRKGTDMYTGTLDCRKRITARDEGKAFKFGKAMSVYLRMGAFVLYVDEIKKY 297
 DB 241 OSGRKGTDMYTGTLDCRKRITARDEGKAFKFGKAMSVYLRMGAFVLYVDEIKKY 297
 RESULT 10
 ADT_DROME STANDARD; PRT; 299 AA.
 AC Q26365; P91614; Q26254; Q95530; Q9VZ70;
 DT 15-0UL-1998 (Rel. 36, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
 DE translocator) (ANT) (Stress sensitive B protein).
 GN SEB8 OR A/A-T OR CG16944.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peerygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92389367; PubMed=1387687;
 RA Louvi A., Tsilioni S.G.;
 RT "A cDNA clone encoding the ADP/ATP translocase of Drosophila
 RT melanogaster shows a high degree of similarity with the mammalian
 RT ADP/ATP translocases".
 RL J. Mol. Evol. 35:44-50(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94350065; PubMed=7520869;
 RA Hutter P., Karch F.;
 RT "Molecular analysis of a candidate gene for the reproductive
 RT isolation between sibling species of Drosophila".
 RL Experientia 50:749-762(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Oregon-R;
 RA Zhang Y.O., Davis A.W., Roote J., Herrmann S., Ashburner M.;
 RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernier B.P., Bhandal D., Bolshakov S.,
 RA Borokova D., Botchan M.A., Boulter J., Brokstein P., Brotter P.,
 RA Butcher K.C., Butman D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fowler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jaitani M., Kalish F., Karpen G.H., Ke Z., Kemtson J.A., Ketchum K.A.,

RA Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mettel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Sider-Kimmo I., Simpson M., Skupski M.P., Smith T.,
 RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun B.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of Drosophila melanogaster.";
 RA Science 287:2185-2195(2000).
 RT [5]
 RN SEQUENCE FROM N.A.
 RP STRAIN-Berkeley; TISSUE-larva, Ovary, and Pupa;
 RC MEDLINE=22426066; PubMed=12537569;
 RX Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
 RA George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
 RA Rubin G.M., Celniker S.B.;
 RA "A Drosophila full-length cDNA resource.";
 RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
 CC -1- FUNCTION: Catalyzes the exchange of ADP and ATP across the
 CC mitochondrial inner membrane.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane (By similarity).
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; S43651; AAB23114.1; -;
 DR EMBL; S71762; AAB31734.3; -;
 DR EMBL; Y10618; CAA71628.1; -;
 DR EMBL; AE003484; AAF47957.1; -;
 DR EMBL; AY060978; AAL28526.1; -;
 DR EMBL; AY070894; AAL48516.1; -;
 DR FLYBase; FBgn0003360; seeb.
 DR GO; GO:0005743; C:mitochondrial inner membrane; IMP.
 DR GO; GO:0006839; P:mitochondrial transport; IMP.
 DR InterPro; IPR002067; Mlt carrier.
 DR InterPro; IPR001993; Mitoch carrier.
 DR Pfam; PF00153; mltc; carr; 2;
 DR PRINTS; PRO0926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 DR KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 14 31 1 (POTENTIAL).
 FT TRANSMEM 75 93 2 (POTENTIAL).
 FT TRANSMEM 119 136 3 (POTENTIAL).
 FT TRANSMEM 177 196 4 (POTENTIAL).
 FT TRANSMEM 215 232 5 (POTENTIAL).
 FT TRANSMEM 274 292 6 (POTENTIAL).
 FT TRANSMEM 18 19 GI -> OV (IN REF. 1 AND 2).
 FT TRANSMEM 81 81 I -> Y (IN REF. 1 AND 2).
 FT TRANSMEM 201 201 MISSING (IN REF. 1 AND 2).
 FT TRANSMEM 267 267 G -> A (IN REF. 2).
 FT TRANSMEM 268 269 TG -> P (IN REF. 1 AND 2).
 FT TRANSMEM 270 270 A -> S (IN REF. 1).
 FT TRANSMEM 270 270 A -> C (IN REF. 2).
 FT TRANSMEM 299 AA; 32909 MM; DS1F3E2A70BD59B8 C6C64;
 SQ SEQUENCE

Query Match 81.0%; Score 1253.5; DB 1; Length 299;
 Best Local Similarity 81.2%; Pred. No. 7,1e-103;
 Matches 237; Conservative 21; Mismatches 33; Indels 1; Gaps 1;
 Oy 5 ALSAPKFLAGVAANAISKTAVARIERYKLLQVQASHKQITADQYKGIIDCVRIKPE 64
 Db 7 AVGFVQKPAAGISAAVSKTAVAIERYKLLQVQASHKQISPDQKQYGMWDFRIRKPE 66
 Oy 65 QEVLSFPMGNLANITRPPPTALNFAFDKTKQIFLGVDVKTQPMFRFAENLASGGAG 124
 Db 67 QGFSSFMGNLANITRPPPTALNFAFDKTKQVFLGVDVKTQPMFRFAENLASGGAG 126
 Oy 125 ATSLCFVPLDPARTPLAADVGKAGSERFGLDCLVKIKSPGKIKLQGFVFNVSVOGI 184
 Db 127 ATSLCFVPLDPARTPLAADVGK -GGQREFTGLNCLTKIKSDGIVGLYGFVSVQGI 185
 Oy 185 ILYRAAYFGIYDPAKGMLPDEKNTHTIVISWNIAGTVTAAGITSPPTVRRMMQSGR 244
 Db 186 ILYRAAYFGIYDPAKGMLPDEKNTHTIVISWNIAGTVTAAGITSPPTVRRMMQSGR 245
 Oy 245 KGTIMTGTITLDCRKTKIARDGGAFFRGANSNVLKMGCAFVLYVDEIKK 296
 Db 246 KATEVIYKNTLHCWATIAKQGTGAFKGFAPSNILRGTGAFVLYVDEIKK 297
 RESULT 11
 ADT-ANOGA STANDARD; PRT; 301 AA.
 ID ADT-ANOGA
 AC Q27238;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE ADP-ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
 DE translocator) (ANT).
 OS Anopheles gambiae (African malaria mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
 CX NCBI_Taxid=7165;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=G3;
 RX MEDLINE=94348635; PubMed=8069414;
 RA Beard C.B., Crews-Oyen A.E., Kumar V.K., Collins F.H.;
 RT "A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles
 RT gambiae.";
 RL Insect Mol. Biol. 3:35-40(1994).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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 CC -----
 CC EMBL; L11618; AAB04104.1; -;
 DR EMBL; L11617; AAB04105.1; -;
 DR InterPro; IPR002067; Mlt carrier.
 DR InterPro; IPR001993; Mitoch carrier.
 DR Pfam; PF00153; mltc; carr; 3;
 DR PRINTS; PRO0926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 DR KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 14 31 1 (POTENTIAL).
 FT TRANSMEM 75 93 2 (POTENTIAL).
 FT TRANSMEM 119 136 3 (POTENTIAL).
 FT TRANSMEM

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FT TRANSMEM 178 197 4 (POTENTIAL).
FT TRANSMEM 216 233 5 (POTENTIAL).
FT TRANSMEM 275 293 6 (POTENTIAL).
SQ SEQUENCE 301 AA; 32863 MW; 4CC9E17C9F8DA08B CRC64;

Query Match
Best Local Similarity 76.9%; Score 1190; DB 1; Length 301;
Matches 227; Conservative 18; Mismatches 43; Indels 0; Gaps 0;

QY 8 FAKDLIAGVAAIAIKTAVAPIERVYLLIQVHASKQIADKQYKGIIDCVRIKPEOV 67
DB 10 FAKDLIAGVAAIAIKTAVAPIERVYLLIQVHASKQIADKQYKGIIDCVRIKPEOV 69
QY 68 LSFWRGNLANVIRYPTQALNFAFKDKYQIFLGVDKRTQWRYPAGNLASGGAAGATS 127
DB 70 GAFWRGNLANVIRYPTQALNFAFKDKYQIFLGVDKRTQWRYPAGNLASGGAAGATS 129
QY 128 LCFVYPLDPARTRLADVGRKAGABERFGLDCLVKIYKSDGIRKLYOGFNVYSGGLIY 187
DB 130 LCFVYPLDPARTRLADVGRKAGABERFGLDCLVKIYKSDGIRKLYOGFNVYSGGLIY 189
QY 188 RAAVGIYDTAKGMLPDPKNTHTIVISWIAQTVAAGLTSYPTDVRERMMQSGRKGT 247
DB 190 RAAVGCCTDTAKGMLPDPKNTHTIVISWIAQTVAAGLTSYPTDVRERMMQSGRKGT 249
QY 248 DIMYTGTLDCWRKIARDGEGKAPFKGAMSNVLRGKGAFLVLYDEIK 295
DB 250 EVMYKNTLDCWVKIKQSGSGAFPFKGAFLVLYDEIK 297

RESULT 12
ADT_CHUNK STANDARD; PRT; 339 AA.
AC P31692;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ADP-ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
translocator) (ANT).
OS Chlorella kesselii.
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
OC Chlorellaceae; Chlorellia.
OX NCBI_TaxId=3074;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=92084708; PubMed=1748677;
RA Hilgarch C., Sauer N., Tanner W.;
RT "Glucose increases the expression of the ATP/ADP translocator and the
glyceroldehyde-3-phosphate dehydrogenase genes in Chlorella.";
RL J. Biol. Chem. 266:24044-24047(1991).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M76669; AAA33027.1; -
CC PIR; A41677; A41677.
CC InterPro; IPR002067; Mlt carrier.
CC InterPro; IPR001993; Mitoch carrier.
CC Pfam; PF00153; mltcarr; 3.
CC PRINTS; PR00926; MITOCARRIER.
CC PROSITE; PS00215; MITOCH_CARRIER; 3.

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KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT TRANSMEM 45 62 1 (POTENTIAL).
FT TRANSMEM 108 126 2 (POTENTIAL).
FT TRANSMEM 151 168 3 (POTENTIAL).
FT TRANSMEM 209 228 4 (POTENTIAL).
FT TRANSMEM 248 265 5 (POTENTIAL).
FT TRANSMEM 304 322 6 (POTENTIAL).
SQ SEQUENCE 339 AA; 36886 MW; 54779734A3B3942 CRC64;

Query Match
Best Local Similarity 62.6%; Score 968; DB 1; Length 339;
Matches 194; Conservative 29; Mismatches 64; Indels 8; Gaps 5;

QY 6 LSFAPDLIAGVAAIAIKTAVAPIERVYLLIQVHASKQIADKQYKGIIDCVRIKPEOV 63
DB 39 MAFVYDLIAGVAAIAIKTAVAPIERVYLLIQVHASKQIADKQYKGIIDCVRIKPEOV 98
QY 64 BOEVLSPFRGNLANVIRYPTQALNFAFKDKYQIFLGVDKRTQWRYPAGNLASGGA 123
DB 99 BOEVLSPFRGNLANVIRYPTQALNFAFKDKYQIFLGVDKRTQWRYPAGNLASGGA 157
QY 124 GATSLCFVYPLDPARTRLADVGRKAGABERFGLDCLVKIYKSDGIRKLYOGFNVYSG 183
DB 158 GATSLCFVYPLDPARTRLADVGRKAGABERFGLDCLVKIYKSDGIRKLYOGFNVYSG 216
QY 184 IIRYRAVGIYDTAKGMLPDPKNTHTIVISWIAQTVAAGLTSYPTDVRERMMQSG 242
DB 217 IIRYRAVGIYDTAKGMLPDPKNTHTIVISWIAQTVAAGLTSYPTDVRERMMQSG 276
QY 243 GRKGTDIMYTGTLDCWRKIARDGEGKAPFKGAMSNVLRGKGAFLVLYDEIK 297
DB 277 ---GGEROYNGIIDCMRKVIARDGEGKAPFKGAMSNVLRGKGAFLVLYDEIK 328

RESULT 13
ADT1_GOSHI STANDARD; PRT; 386 AA.
AC O22342;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADP-ATP carrier protein 1, mitochondrial precursor (ADP/ATP
translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
OS Arabidopsis thaliana (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eusteroideae; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxId=3635;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. Texas Marker 1; TISSUE=Fiber;
RA Shin H., Brown R.M. Jr.;
RT "Two cDNA sequences for the adenine nucleotide translocator, CANT1 and
CANT2, from cotton fibers (Gossypium hirsutum).";
RL (In) Plant Gene Register PGR97-130.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
inner membrane (By similarity).
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF006489; AAB72047.1; -
CC PIR; T09709; T09709.
CC InterPro; IPR002067; Mlt carrier.
CC InterPro; IPR001993; Mitoch carrier.
CC Pfam; PF00153; mltcarr; 3.

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DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH CARRIER; 2.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Transmembrane; Multigene family.
 FT TRANSIT 1
 FT TRANSIT 76
 FT TRANSIT 77
 FT TRANSIT 90
 FT TRANSIT 107
 FT TRANSIT 152
 FT TRANSIT 170
 FT TRANSIT 195
 FT TRANSIT 212
 FT TRANSIT 256
 FT TRANSIT 275
 FT TRANSIT 295
 FT TRANSIT 312
 FT TRANSIT 351
 FT TRANSIT 369
 FT TRANSIT 42093 MW; A05F76C73FECDE6 CRC64;
 SQ SEQUENCE 386 AA; 42093 MW; A05F76C73FECDE6 CRC64;
 Query Match 49.8%; Score 771; DB 1; Length 386;
 Best Local Similarity 53.4%; Pred. No. 2.3e-60;
 Matches 169; Conservative 35; Mismatches 79; Indels 22; Gaps 7;
 QY 7 SPANFLAGVAAIASTAVAPIERVKLLQVQ--HASKQTADKQYGIIDCVIRPKQ 65
 DB 85 SPALDFLMGVSAAVSKTAAPIERVKLLQVQ--HASKQTADKQYGIIDCVIRPKQ 144
 QY 66 EVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLAAGGA 125
 DB 145 GFGSLMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLAAGGA 203
 QY 126 TSLCVVYLDPAFTLADV--GKAGAREFRGLDCLVKYKSGIKGLYQGFVNSVQ 183
 DB 204 SLLFVYSLDPAFTLADV--GKAGAREFRGLDCLVKYKSGIKGLYQGFVNSVQ 263
 QY 184 IIVYRAVFGIYDPAK-----GMLPDKNTNIVISMTIAQTAVAGLTSYPTVRRM 238
 DB 264 IIVYRAVFGIYDPAK-----GMLPDKNTNIVISMTIAQTAVAGLTSYPTVRRM 319
 QY 239 MMSGRKKTIDMYTGLDCKRRIARDEGKAFKAGMNSVLRGMGAFVLYDEI---- 294
 DB 320 MMSGRKKTIDMYTGLDCKRRIARDEGKAFKAGMNSVLRGMGAFVLYDEI---- 376
 QY 295 --KKY 297
 DB 377 FGKXY 381
 RESULT 14
 ADT_SCHPO STANDARD; PRT; 322 AA.
 AC Q09188;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).
 GN ANCL OR SPBC530.10C.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 CC Schizosaccharomycetales; Schizosaccharomycetaceae;
 CC Schizosaccharomycetes.
 CX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=96257204; PubMed=8675018;
 RA Cousin N., Trezeguet V., Sauk A.L., Lauguin G.J.M.;
 RT "Cloning of the gene encoding the mitochondrial adenine nucleotide carrier of Schizosaccharomycetes pombe by functional complementation in Saccharomyces cerevisiae.";
 RL Gene 171:113-117(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Brooke K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Stevens S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Voicikert G., Aert R., Roben J., Grymopiez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritz C., Holzer B., Moesl D., Hilbert H., Borzym K., Langer I., Beck A., Lebrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Medler H., Wandt R., Punelle B., Goffeau A., Cadieu B., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert P., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Rhode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Useery D., Bartell B.G., Nurse P.;
 RA "The genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880(2002).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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 CC -----
 DR EMBL; Z49974; CA90275.1; -.
 DR EMBL; AL023634; CA919176.1; -.
 DR PIR; T40526; T40526.
 DR GeneDB; SPBC530.10C; -.
 DR InterPro; IPR002067; Mlt_carrier.
 DR InterPro; IPR001993; Mltch_carrier.
 DR Pfam; PF00153; mltc_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH CARRIER; 2.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSIT 28
 FT TRANSIT 48
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 FT TRANSIT 111
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 FT TRANSIT 197
 FT TRANSIT 217
 FT TRANSIT 242
 FT TRANSIT 289
 FT TRANSIT 309
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 SQ SEQUENCE 322 AA; 35020 MW; BAC3D16A40F41AFC CRC64;
 Query Match 49.8%; Score 770; DB 1; Length 322;
 Best Local Similarity 53.6%; Pred. No. 2.3e-60;
 Matches 158; Conservative 51; Mismatches 74; Indels 12; Gaps 6;
 QY 7 SPANFLAGVAAIASTAVAPIERVKLLQVQ--HASKQTADKQYGIIDCVIRPK 63
 DB 26 TFPDFPMGVSAAVSKTAAPIERVKLLQVQ--DEMIRAGLSHYKGIIDCVIRPK 83
 QY 64 EOVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLAAGGA 123
 DB 84 BEGVLSMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLAAGGA 142
 QY 124 GATSLCVVYLDPAFTLADV--GKAGAREFRGLDCLVKYKSGIKGLYQGFVNSV 181
 DB 143 GAASLVLVYSLDPAFTLADV--GKAGAREFRGLDCLVKYKSGIKGLYQGFVNSV 202

Qy 182 QGIIYRAAYFGIYDTAKG-MLPDPKNTHTIVISMIAGTVTAAGLTSYPTVRRMM 240
 Db 203 VGIIVYRGILYFGMYDVLKPVVLVGPLBGNFLASFLGAVMTTGSVASYPLDITRRMM 262
 Qy 241 QSGRGDTIMYGTLDCKWKIARDGKAFFGAGSNVLRGNGAFVLYLDEIK 295
 Db 263 TSGEA---VKYSSFECCGRQILAKGARSFFGAGANNILRGVAGAGVLSYDQV 314

RESULT 15

ADT_CHIRE STANDARD; PRT; 308 AA.

AC P27080;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE ADP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).
 GN ABT.
 OS Chlamydomonas reinhardtii.
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 CC Chlamydomonadaceae; Chlamydomonas.
 OX NCBI_TaxID=3055;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FUD4-R2;
 RX MEDLINE=93204887; PubMed=8455552;
 RA Sharpe J.A., Day A.;
 RT "Structure, evolution and expression of the mitochondrial ADP/ATP translocator gene from Chlamydomonas reinhardtii.",
 RL Mol. Gen. Genet. 237:134-144(1993).
 CC -1 FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1 SUBUNIT: Homodimer.
 CC -1 SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
 CC -1 DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1 SIMILARITY: Belongs to the mitochondrial carrier family.

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 CC -----
 DR EMBL; X65194; CAA46311.1; -.
 DR PIR; S30259; S30259.
 DR InterPro; IPR002067; Mtc carrier.
 DR InterPro; IPR001993; MitoCh carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 2.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 74 92 2 (POTENTIAL).
 FT TRANSMEM 116 133 3 (POTENTIAL).
 FT TRANSMEM 178 197 4 (POTENTIAL).
 FT TRANSMEM 217 234 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 SQ SEQUENCE 308 AA; 33528 MW; D477CF0E72B7A53F CRC64;

Query Match 49.5%; Score 765; DB 1; Length 308;

Best Local Similarity 52.6%; Pred. No. 66-60; 78; Indels 16; Gaps 6;
 Matches 159; Conservative 49; Mismatches 78; Indels 16; Gaps 6;

Qy 7 SPKADFLAGVAAAIKSTVAPIERVKLLQVQ-HASKQITADKQYKGIIDCVRIPEKQ 65
 Db 7 NFMVDFLAGGSAASKTAAPIERVKLLIQNDEMIRKGRSLAPYKGIQECFVTVREE 66
 Qy 66 EYLSFWRGNLAVNIYFPFQALNPAFKQIKQIFLGVDKTFQFWRYFAGNLASGGAAGA 125

Db 67 GFGLMRNTANVNIYFPFQALNPAFKQIKQMF--GNKQKTIWKFAGNASGGAAGA 124
 Qy 126 TSLCFVYPLDPAKTRTLAD---VGKAGAEERFGRGDCIVYIKSDGIRGLYQGFNVSVQ 182
 Db 125 VLSFVYSLDVARTRTLANDASAKKGGDRQFNGLVVDYRKTIASDGIAGIRGFNISCY 184
 Qy 183 GIITYRAAYFGIYDTAKG-MLPDPKNTHTIVISMIAGTVTAAGLTSYPTVRRMMQ 241
 Db 185 GIVYRGILYFGMYDVLKPVVLVGPLANNFLAFLGWIITIGAGLASYPIDITRRMMWT 244
 Qy 242 SGRKGTIMYGTLDCKWKIARDGKAFFGAGSNVLRGNGAFVLYLDEI-----K 295
 Db 245 S---GSAVKINSFRCFQEIYKNGSKSLFKGAGANNILRAVAGAGVLAGYDQLQYIILGK 301
 Qy 296 KY 297
 Db 302 KY 303

Search completed: December 18, 2003, 12:41:24
 Job time : 9.34267 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:34:56 ; Search time 35.3729 Seconds
(without alignments)
1337.197 Million cell updates/sec

Title: US-09-811-131-33

Perfect score: 1543

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Scoring table:

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Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	100.0	298	21	AAV71033
2	1543	100.0	298	22	AAV71033
3	1543	100.0	298	22	AAU01200
4	1543	100.0	298	23	AAU01380
5	1543	100.0	298	23	AAU01427
6	1463	94.8	298	23	AAO18516
7	1454	94.2	298	21	AAV71032
8	1454	94.2	298	22	AAU01199
9	1454	94.2	298	23	AAU01379

10	1418	91.9	429	24	ABR41715	Human DITRP organe
11	1412	91.5	298	19	AAK61169	Anti protein. Mus
12	1406	91.1	293	22	ABU3219	Human metabolism-a
13	1385.5	89.8	297	21	AAV71031	Human adenine nucl
14	1385.5	89.8	297	23	AAU01198	Human adenine nucl
15	1385.5	89.8	297	23	AAU01378	Human adenine nucl
16	1367.5	88.6	325	22	ABG15423	Novel human diagno
17	1288	83.5	263	22	ABG37056	Novel human diagno
18	1254.5	81.3	299	22	ABBE6082	Drosophila melanog
19	1254.5	81.3	299	22	ABBE7300	Drosophila melanog
20	1137.5	73.7	307	22	ABBE58380	Human metabolism-a
21	1119	72.5	315	23	ABU53218	Human TRIC-19 pro
22	1119	72.5	315	23	ABE21175	Human TRIC-19 pro
23	1044	67.7	228	23	ABP43205	Human ovarian anti
24	981	63.6	222	23	ABP74106	Human TRIC-19 pro
25	879.5	57.0	298	22	ABG18922	Novel human diagno
26	788.5	51.1	301	23	ABP73357	Candida albicans e
27	763	49.4	484	22	ABG15422	Novel human diagno
28	763	49.4	484	22	ABG37055	Novel human diagno
29	749.5	48.6	386	22	AAU0106	ADP/ATP carrier pr
30	743	48.2	379	24	ABP81267	Arabidopsis thalia
31	742.5	48.1	346	21	AAU36577	Arabidopsis thalia
32	742.5	48.1	346	21	AAU37261	Arabidopsis thalia
33	742.5	48.1	346	21	AAU37264	Arabidopsis thalia
34	742.5	48.1	346	21	AAU38460	Arabidopsis thalia
35	742.5	48.1	363	21	AAU36576	Arabidopsis thalia
36	742.5	48.1	363	21	AAU37260	Arabidopsis thalia
37	742.5	48.1	363	21	AAU37263	Arabidopsis thalia
38	742.5	48.1	363	21	AAU38459	Arabidopsis thalia
39	742.5	48.1	381	21	AAU36575	Arabidopsis thalia
40	742.5	48.1	381	21	AAU37259	Arabidopsis thalia
41	742.5	48.1	381	21	AAU37262	Arabidopsis thalia
42	742.5	48.1	381	21	AAU38458	Arabidopsis thalia
43	742.5	48.1	992	21	AAU38671	Arabidopsis thalia
44	742.5	48.1	1009	21	AAU38672	Arabidopsis thalia
45	742.5	48.1	1027	21	AAU38670	Arabidopsis thalia

ALIGNMENTS

RESULT 1	AAV71033	standard; Protein; 298 AA.
ID	AAV71033	
XX	AAV71033	
AC	AAV71033	
XX	AAV71033	
DT	29-AUG-2000	(first entry)
XX	29-AUG-2000	
DB	Human adenine nucleotide translocator ANT3.	
XX	Human, adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;	
KW	adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MP; cancer;	
KW	mitochondrial permeability transition; neuroprotective; neurotrophic;	
KW	antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;	
KW	antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;	
KW	Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;	
KW	diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;	
KW	mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;	
KW	mitochondrial diabetes and deafness; hyperepileptic disorder;	
KW	myoclonic epilepsy red ragged fibre syndrome.	
XX		
OS	Homo sapiens.	
XX		
PN	W0200026370-A2.	
XX		
PD	11-MAY-2000.	
XX		
XX	03-NOV-1999;	99WO-US25863.
XX		
XX	03-NOV-1998;	98US-0185904.
PR	08-SEP-1999;	99US-0393441.
XX		

PA (MITO-) MITOKOR.
 XX
 PI Anderson CM, Davis RE, Clevenger W, Wiley SB, Miller SM, Szabo TR,
 PI Ghosh SS,
 XX WPI, 2000-365619/31.
 DR N-PSDB; AAD00521.
 XX
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 XX
 PS Claim 46, Page 173-174, 175pp; English.
 XX
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT3 from human brain.
 CC
 XX
 SQ Sequence 298 AA;
 XX
 Query Match 100.0%; Score 1543; DB 21; Length 298;
 Best Local Similarity 100.0%; Pred. No. 4.6e-157;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 MTEQAIISFAKDFLAGGIAAISKTAIVAPIERVKLLQVQHASKOIADKQYGIYDCIVR 60
 DB 1 MTEQAIISFAKDFLAGGIAAISKTAIVAPIERVKLLQVQHASKOIADKQYGIYDCIVR 60
 QY 61 IPKEQGVLSFWRGNLANIYRFPPTQALNPAFDKTKQIFLGVDVHTQTFWRYPAGNLASG 120
 DB 61 IPKEQGVLSFWRGNLANIYRFPPTQALNPAFDKTKQIFLGVDVHTQTFWRYPAGNLASG 120
 QY 61 IPKEQGVLSFWRGNLANIYRFPPTQALNPAFDKTKQIFLGVDVHTQTFWRYPAGNLASG 120
 DB 61 IPKEQGVLSFWRGNLANIYRFPPTQALNPAFDKTKQIFLGVDVHTQTFWRYPAGNLASG 120
 QY 121 GAAGATSLCFYVPLDPFARTRLAADVGKSTGERFGLDCLVKTKSGIRGLYQGFVS 180
 DB 121 GAAGATSLCFYVPLDPFARTRLAADVGKSTGERFGLDCLVKTKSGIRGLYQGFVS 180
 QY 181 VGGIITVRAAFVGYVDTAKGMLPDPKNTIHIVSWMIAQTVAIVAGVSYFPDVARMM 240
 DB 181 VGGIITVRAAFVGYVDTAKGMLPDPKNTIHIVSWMIAQTVAIVAGVSYFPDVARMM 240
 QY 241 OSGRGADIMYGTGTDCKRKIRIRDEGKAFPGKANSNVRGKGAFLVLYBELKKVI 298
 DB 241 OSGRGADIMYGTGTDCKRKIRIRDEGKAFPGKANSNVRGKGAFLVLYBELKKVI 298
 XX
 RESULT 2
 AAM39641
 ID AAM39641 standard; Protein; 298 AA.
 XX
 AC AAM39641;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 2786.
 XX
 DE Human; nocrotic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000WO-US34263.
 XX
 PR 21-JAN-2000; 2000US-0498725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao Q, Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI, 2001-442253/47.
 DR N-PSDB; AAI58797.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX
 PS Example 4; SEQ ID NO 2786; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AA15798-AA161369) and
 CC the encoded polypeptides (AAM3642-AAM42213) with nocrotic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localized neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilization of the activities such as: immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemia and
 CC C.N.S disorders
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 CC
 XX
 SQ Sequence 298 AA;
 XX
 Query Match 100.0%; Score 1543; DB 22; Length 298;
 Best Local Similarity 100.0%; Pred. No. 4.6e-157;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 MTEQAIISFAKDFLAGGIAAISKTAIVAPIERVKLLQVQHASKOIADKQYGIYDCIVR 60
 DB 1 MTEQAIISFAKDFLAGGIAAISKTAIVAPIERVKLLQVQHASKOIADKQYGIYDCIVR 60
 QY 61 IPKEQGVLSFWRGNLANIYRFPPTQALNPAFDKTKQIFLGVDVHTQTFWRYPAGNLASG 120
 DB 61 IPKEQGVLSFWRGNLANIYRFPPTQALNPAFDKTKQIFLGVDVHTQTFWRYPAGNLASG 120
 QY 61 IPKEQGVLSFWRGNLANIYRFPPTQALNPAFDKTKQIFLGVDVHTQTFWRYPAGNLASG 120
 DB 61 IPKEQGVLSFWRGNLANIYRFPPTQALNPAFDKTKQIFLGVDVHTQTFWRYPAGNLASG 120
 QY 121 GAAGATSLCFYVPLDPFARTRLAADVGKSTGERFGLDCLVKTKSGIRGLYQGFVS 180
 DB 121 GAAGATSLCFYVPLDPFARTRLAADVGKSTGERFGLDCLVKTKSGIRGLYQGFVS 180
 QY 181 VGGIITVRAAFVGYVDTAKGMLPDPKNTIHIVSWMIAQTVAIVAGVSYFPDVARMM 240
 DB 181 VGGIITVRAAFVGYVDTAKGMLPDPKNTIHIVSWMIAQTVAIVAGVSYFPDVARMM 240
 QY 241 OSGRGADIMYGTGTDCKRKIRIRDEGKAFPGKANSNVRGKGAFLVLYBELKKVI 298
 DB 241 OSGRGADIMYGTGTDCKRKIRIRDEGKAFPGKANSNVRGKGAFLVLYBELKKVI 298

Qy 241 QSGRGADIMVTGVDGCRKIFRDEGKAPFGKAMSVLRMGAFVLYDELKVI 298
 Db 241 QSGRGADIMVTGVDGCRKIFRDEGKAPFGKAMSVLRMGAFVLYDELKVI 298

RESULT 3
 ID AAU01200 standard; Protein; 298 AA.
 AC AAU01200;
 XX
 XX 07-SEP-2001 (first entry)
 DT
 XX
 DE Human adenine nucleotide translocator-3 (ANT-3) protein.
 XX
 KW Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX
 OS Homo sapiens.
 PN WO200132876-A2.
 PD 10-MAY-2001.
 XX
 PE 03-NOV-2000; 2000WO-US30535.
 PR 03-NOV-1999; 99US-0434354.
 PA (MITO-) MITOKOR.
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AV, Frigeri LG;
 PI Veilcelabl G, Davis RE;
 DR MPI; 2001-291054/30.
 DR N-PSDB; AAS05903.
 XX
 PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 PS Disclosure; Fig 2; 186pp; English.

The present sequence represents human adenine nucleotide translocator-3 (ANT-3) protein. ANT proteins are mitochondrial permeability transition (MPT) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to regulate MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. green fluorescent protein (GFP) or a FLAISH sequence). The novel expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MPT and/or cell survival. These agents are useful for the prevention or treatment of diseases associated with altered mitochondrial function or dysfunction of cell survival, such as Alzheimer's disease, diabetes mellitus, Parkinson's disease, Huntington's disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke, hyperproliferative disorders e.g. cancer, and deafness.

Sequence 298 AA;
 Query Match 100.0%; Score 1543; DB 22; Length 298;
 Best Local Similarity 100.0%; Pred. No. 4.6e-157;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MTEQAISPAKDFLAGIAAIAISKTAVPIERVKLLQVQHASKOIAADKQKGYVDCIVR 60
 |||
 |||

Db 1 MTEQAISPAKDFLAGIAAIAISKTAVPIERVKLLQVQHASKOIAADKQKGYVDCIVR 60
 Qy 61 IPKQGLTSPFRGLAVIRPFPQALNFAKDKYKQIFLGVDNKHQPFMYEPGNLASG 120
 Db 61 IPKQGLTSPFRGLAVIRPFPQALNFAKDKYKQIFLGVDNKHQPFMYEPGNLASG 120
 Qy 121 GAAGTSLCFYPPDPARTRLAADVSGSTGERFRGLDCLVKTGSDIGRLYQGFSEVS 180
 Db 121 GAAGTSLCFYPPDPARTRLAADVSGSTGERFRGLDCLVKTGSDIGRLYQGFSEVS 180
 Qy 181 VQGIITRYRAAYFGVYDTAKGMLPDPKXTHIVSWMLAQVTVAVGVSYPPDTRRRMM 240
 Db 181 VQGIITRYRAAYFGVYDTAKGMLPDPKXTHIVSWMLAQVTVAVGVSYPPDTRRRMM 240

Qy 241 QSGRGADIMVTGVDGCRKIFRDEGKAPFGKAMSVLRMGAFVLYDELKVI 298
 Db 241 QSGRGADIMVTGVDGCRKIFRDEGKAPFGKAMSVLRMGAFVLYDELKVI 298

RESULT 4
 ID AAU0380 standard; Protein; 298 AA.
 AC AAU0380;
 XX
 XX 14-FEB-2002 (first entry)
 DT
 XX
 DE Human adenine nucleotide translocator 3 (ANT3).
 XX
 KW Human; adenine nucleotide translocator; ANT;
 KW mitochondrial matrix protein.
 XX
 OS Homo sapiens.
 PN WO200185944-A2.
 PD 15-NOV-2001.
 XX
 PE 11-MAY-2001; 2001WO-US15416.
 PR 11-MAY-2000; 2000US-0569327.
 PA (MITO-) MITOKOR.
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS, Moos WH, Pei Y, Carroll AK;
 DR MPI; 2002-055598/07.
 DR N-PSDB; AAS16690.
 XX
 PT Novel recombinant expression construct for producing adenine nucleotide
 PT translocator polypeptides, comprises a regulated promoter linked to
 PT nucleic acid encoding the polypeptide -
 PS Example 3; Fig 2; 147pp; English.

The invention relates to a recombinant expression construct (I) comprising a regulated promoter operably linked to a nucleic acid encoding an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesised in the mitochondrial matrix for ADP in the cytosol. (I) is useful for producing recombinant ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and culturing the host cell. (I) is also useful for targeting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is expressed as a fusion protein with the polypeptide of interest. Recombinant ANT polypeptide, or cells expressing the polypeptide, is useful for identifying an agent that binds to an ANT polypeptide. ANT ligand is useful for determining the presence of an ANT polypeptide, preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating ANT from a biological sample, where the ANT ligand is covalently or non-covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. The present sequence represents the amino acid sequence of human ANT3.

XX SQ Sequence 298 AA;
 Query Match 100.0%; Score 1543; DB 23; Length 298;
 Best Local Similarity 100.0%; Pred. No. 4,6e-157;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQAIISPAKDFLAGGIAAAISKTAVAPIERVKLLQVQHASKQIAADKQYKGIYDCIVR 60
 DB 1 MTEQAIISPAKDFLAGGIAAAISKTAVAPIERVKLLQVQHASKQIAADKQYKGIYDCIVR 60
 QY 61 IPKEQGVLSFWRGNLANVIRFPYQALNFAFKDKYKQIFLGVDVGHQTFWRFPAGNLASG 120
 DB 61 IPKEQGVLSFWRGNLANVIRFPYQALNFAFKDKYKQIFLGVDVGHQTFWRFPAGNLASG 120
 QY 121 GAAGATSLCFYVPLDFARTRLAADVKGSGTEREFRLGDCLVKTKSGIRGLYQGFVSYS 180
 DB 121 GAAGATSLCFYVPLDFARTRLAADVKGSGTEREFRLGDCLVKTKSGIRGLYQGFVSYS 180
 QY 181 VQGIITVRAAYFGVYDTAKGMLPDPKXTHIVSWMIAQTVTAVAGVVSYPDVTARRMM 240
 DB 181 VQGIITVRAAYFGVYDTAKGMLPDPKXTHIVSWMIAQTVTAVAGVVSYPDVTARRMM 240
 QY 241 QSGRGKADIMYTGIVDCWRKIFRDEGGKAFPKGAMSNVLRMGGAFLVLYDELKCVI 298
 DB 241 QSGRGKADIMYTGIVDCWRKIFRDEGGKAFPKGAMSNVLRMGGAFLVLYDELKCVI 298

RESULT 5
 AAM41427 standard; Protein; 323 AA.
 AAM41427;
 XX 22-OCT-2001 (first entry)
 DT Human polypeptide SEQ ID NO 6358.
 DE
 XX Human; nocotropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokine; chromolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 KW
 XX Homo sapiens.
 OS
 XX WO200153312-A1.
 PN
 XX 26-JUL-2001.
 PD
 XX 26-DEC-2000; 2000WO-US34263.
 PF
 XX 21-JAN-2000; 2000US-0486725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 PR
 XX (HYSE-) HYSEQ INC.
 PA
 XX Tang YF, Liu C, Aundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao Q, Zhou P, Goodrich R, Drmanac RT;
 XX WPI; 2001-442253/47.
 DR N-PSDB; AAI60583.
 XX Novel nucleic acids and polypeptides; useful for treating disorders
 PT such as central nervous system injuries -

XX SQ Sequence 323 AA;
 Query Match 100.0%; Score 1543; DB 22; Length 323;
 Best Local Similarity 100.0%; Pred. No. 5,2e-157;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQAIISPAKDFLAGGIAAAISKTAVAPIERVKLLQVQHASKQIAADKQYKGIYDCIVR 60
 DB 26 MTEQAIISPAKDFLAGGIAAAISKTAVAPIERVKLLQVQHASKQIAADKQYKGIYDCIVR 85
 QY 61 IPKEQGVLSFWRGNLANVIRFPYQALNFAFKDKYKQIFLGVDVGHQTFWRFPAGNLASG 120
 DB 86 IPKEQGVLSFWRGNLANVIRFPYQALNFAFKDKYKQIFLGVDVGHQTFWRFPAGNLASG 145
 QY 121 GAAGATSLCFYVPLDFARTRLAADVKGSGTEREFRLGDCLVKTKSGIRGLYQGFVSYS 180
 DB 146 GAAGATSLCFYVPLDFARTRLAADVKGSGTEREFRLGDCLVKTKSGIRGLYQGFVSYS 205
 QY 181 VQGIITVRAAYFGVYDTAKGMLPDPKXTHIVSWMIAQTVTAVAGVVSYPDVTARRMM 240
 DB 206 VQGIITVRAAYFGVYDTAKGMLPDPKXTHIVSWMIAQTVTAVAGVVSYPDVTARRMM 265
 QY 241 QSGRGKADIMYTGIVDCWRKIFRDEGGKAFPKGAMSNVLRMGGAFLVLYDELKCVI 298
 DB 266 QSGRGKADIMYTGIVDCWRKIFRDEGGKAFPKGAMSNVLRMGGAFLVLYDELKCVI 323

RESULT 6
 AAO18516 standard; Protein; 298 AA.
 AAO18516;
 XX 11-OCT-2002 (first entry)
 DT Human insulin receptor signaling modifier SEQ ID NO: 54.
 DE Human insulin receptor signaling modifier; insulin receptor signaling modifier;
 KW human; insulin receptor signaling; insulin receptor signaling modifier;
 KW ISM; diabetes; metabolic syndrome; antidiabetic.
 KW
 XX Homo sapiens.
 OS
 XX WO200255664-A2.
 PN
 XX 18-JUL-2002.
 PD
 XX 11-JAN-2002; 2002WO-US01048.
 PF
 XX 12-JAN-2001; 2001US-261226P.
 PR 12-JAN-2001; 2001US-261303P.
 PR 12-JAN-2001; 2001US-261304P.
 PR 12-JAN-2001; 2001US-261335P.
 PR 12-JAN-2001; 2001US-261336P.

PR 12-JAN-2001; 2001US-261361P.
 PR 12-JAN-2001; 2001US-261456P.
 PR 12-JAN-2001; 2001US-261457P.
 PR 12-JAN-2001; 2001US-261458P.
 PR 12-JAN-2001; 2001US-261459P.
 PR 12-JAN-2001; 2001US-261461P.
 PR 12-JAN-2001; 2001US-261518P.
 PR 12-JAN-2001; 2001US-261531P.
 PR 12-JAN-2001; 2001US-261532P.
 PR 12-JAN-2001; 2001US-261589P.
 PR 12-JAN-2001; 2001US-261590P.
 PR 12-JAN-2001; 2001US-261694P.
 PR 12-JAN-2001; 2001US-261695P.
 PR 12-JAN-2001; 2001US-261697P.
 XX (EXBL-) EXBLIXIS INC.
 PA Seidel-Dugan C, Ferguson KC, Kidd T,
 PI WPI; 2002-599664/64.
 DR N-PSDB; AAL46635.
 XX
 PT Identifying an insulin receptor signaling modulator, useful as drug
 PT targets for treating diabetes or metabolic disorders, comprises
 PT contacting an assay system comprising insulin receptor signaling
 PT modifiers with a test agent -
 XX
 PS Disclosure; Page 160-161; 232pp; English.
 XX
 CC The present invention relates to a method of identifying a candidate
 CC insulin receptor (INR) signaling modulating agent, involving contacting
 CC an assay system comprising an insulin receptor signaling modifier (ISM)
 CC polypeptide or nucleic acid with a test agent, and detecting a test
 CC agent-biased activity of the assay system. The method is useful for
 CC identifying candidate INR signaling modulating agents. ISM genes may be
 CC used as drug targets for treatment of disorders related to INR signaling
 CC such as diabetes or metabolic syndrome. ISM nucleic acids and
 CC polypeptides are useful for identifying and testing agents that modulate
 CC INR function and for other applications related to the involvement of INR
 CC in INR signaling, and for identifying subjects having a predisposition to
 CC such diseases associated with INR signaling. The present sequence is an
 CC ISM protein described in the exemplification of the invention.
 XX
 SQ Sequence 298 AA;
 Query Match 94.8%; Score 1463; DB 23; Length 298;
 Best Local Similarity 92.9%; Pred. No. 1.8e-148;
 Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MTEQALISFADPFLAGGIAAISTKAVAPIERVKLLQVQHSKQIADKQYGVDCIVR 60
 DB 1 MTDAAVSPADPFLAGGIAAISTKAVAPIERVKLLQVQHSKQIADKQYGVDCIVR 60
 QY 61 IPKEGVLSFWRGNLANVIRYPTQALNFAFDKXKQIFLGVDKHTQFMRYFAGNLASG 120
 DB 61 IPKEGVLSFWRGNLANVIRYPTQALNFAFDKXKQIFLGVDKHTQFMRYFAGNLASG 120
 QY 121 GAAAGTSLCFYVPLDPARTRLAADVKGSGTEREFGGLDCLVKTISDGIKGLYOGFSEVS 180
 DB 121 GAAAGTSLCFYVPLDPARTRLAADVKGSGTEREFGGLDCLVKTISDGIKGLYOGFSEVS 180
 QY 181 VOGIITIAAAYFGVVDPAKGMPLDPKNTNTHIVSNMIAQTVAVALTSPDYARRRMM 240
 DB 181 VOGIITIAAAYFGVVDPAKGMPLDPKNTNTHIVSNMIAQTVAVALTSPDYARRRMM 240
 QY 241 QSGRGADIMTGTVCWRKIIFRDEGKAFKFGAANSNVLKRGGAFLVLYDELKK 296
 DB 241 QSGRGADIMTGTVCWRKIIFRDEGKAFKFGAANSNVLKRGGAFLVLYDELKK 296
 RESULT 7
 AA71032
 ID AA71032 standard; Protein; 298 AA.

XX
 AC AA71032;
 XX
 DT 29-AUG-2000 (first entry)
 XX
 DE Human adenine nucleotide translocator ANT2.
 XX
 KW Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP;
 KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
 KW mitochondrial permeability transition; neuroprotective; neurotropic;
 KW antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
 KW antipsychotic; cerebroprotective; therapeutic; screening; psoriasis;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
 KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
 KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
 KW mitochondrial diabetes and deafness; hyperproliferative disorder;
 KW myoclonic epilepsy red ragged fibre syndrome.
 XX
 OS Homo sapiens.
 XX
 XX WO200026370-A2.
 XX
 XX 11-MAY-2000.
 XX
 XX 03-NOV-1999; 99WO-US25863.
 XX
 XX 03-NOV-1998; 98US-0185904.
 XX
 XX 08-SEP-1999; 99US-0393441.
 XX
 XX (MITO-) MITOKOR.
 XX
 XX Anderson CM, Davis RE, Cleverger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh S;
 DR WPI; 2000-365619/31.
 XX N-PSDB; AAD00520.
 XX
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 XX
 PS Claim 45; Page 172-173; 175pp; English.
 XX
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression of
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT2 from human brain.
 XX
 SQ Sequence 298 AA;
 Query Match 94.2%; Score 1454; DB 21; Length 298;
 Best Local Similarity 92.6%; Pred. No. 1.7e-147;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MTEQALISFADPFLAGGIAAISTKAVAPIERVKLLQVQHSKQIADKQYGVDCIVR 60
 DB 1 MTDAAVSPADPFLAGGIAAISTKAVAPIERVKLLQVQHSKQIADKQYGVDCIVR 60
 QY 61 IPKEGVLSFWRGNLANVIRYPTQALNFAFDKXKQIFLGVDKHTQFMRYFAGNLASG 120

Db 61 IPKEGVLSFWKGNLANVIRFPPTQALNFAFKDKTKQIFLGVDKRTQFWRYPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDPFARTRLAADVGKSGTEREFGDGLVKTISDGINGLYOGFSVS 180
 Db 121 GAAGATSLCFVYPLDPFARTRLAADVGKGAERERFGDGLVKTISDGINGLYOGFSVS 180
 QY 181 VGGIITRYAAVFGYDTAKGMLPDPKNTHTIVISWMIAGTVTAAGVSPPTVRRRMM 240
 Db 181 VGGIITRYAAVFGYDTAKGMLPDPKNTHTIVISWMIAGTVTAAGVSPPTVRRRMM 240
 QY 241 QSGRKGADIMTGTVDCKRKIFRDEGKAFPKGAMSNVLRMGAFVLVYDELAK 296
 Db 241 QSGRKGADIMTGTVDCKRKIFRDEGKAFPKGAMSNVLRMGAFVLVYDELAK 296

RESULT 8

AAU01199
 ID AAU01199 standard; Protein; 298 AA.

AC AAU01199;
 DT 07-SEP-2001 (first entry)

DE Human adenine nucleotide translocator-2 (ANT-2) protein.

KM Human; adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;
 KM mitochondrial permeability transition pore component; cell survival;
 KM mitochondrial core component; mitochondrial related disorder; cancer;
 KM Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

OS Homo sapiens.

PN WO200132876-A2.

PD 10-MAY-2001.

PF 03-NOV-2000; 2000MO-US30535.

PR 03-NOV-1999; 99US-0434354.

PA (MITO-) MITOKOR.

PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
 PI Velicelebi G, Davis RB;

DR MPI; 2001-291054/30.

DR N-PSDB; AAS05902.

PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 PS Disclosure; Fig 2; 186pp; English.

CC The present sequence represents human adenine nucleotide translocator-2
 CC (ANT-2) protein. ANT proteins are mitochondrial permeability
 CC transition (MTP) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLAISH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,

CC hyperproliferative disorders e.g. cancer, and deafness.

XX SQ Sequence 298 AA;

Query Match 94.2%; Score 1454; DB 22; Length 298;
 Best Local Similarity 92.6%; Pred. No. 1.7e-147;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEQALSPADKPLAGGIAAIAISKTAVABIEVKLLQVQASKOIADQKQIVDCTVR 60

Db 1 MTDALSPADKPLAGGVAIAISKTAVABIEVKLLQVQASKOIADQKQIVDCTVR 60

QY 61 IPKEGVLSFWKGNLANVIRFPPTQALNFAFKDKTKQIFLGVDKRTQFWRYPAGNLASG 120

Db 61 IPKEGVLSFWKGNLANVIRFPPTQALNFAFKDKTKQIFLGVDKRTQFWRYPAGNLASG 120

QY 121 GAAGATSLCFVYPLDPFARTRLAADVGKSGTEREFGDGLVKTISDGINGLYOGFSVS 180

Db 121 GAAGATSLCFVYPLDPFARTRLAADVGKGAERERFGDGLVKTISDGINGLYOGFSVS 180

QY 181 VGGIITRYAAVFGYDTAKGMLPDPKNTHTIVISWMIAGTVTAAGVSPPTVRRRMM 240

Db 181 VGGIITRYAAVFGYDTAKGMLPDPKNTHTIVISWMIAGTVTAAGVSPPTVRRRMM 240

QY 241 QSGRKGADIMTGTVDCKRKIFRDEGKAFPKGAMSNVLRMGAFVLVYDELAK 296

Db 241 QSGRKGADIMTGTVDCKRKIFRDEGKAFPKGAMSNVLRMGAFVLVYDELAK 296

RESULT 9

AAU0379
 ID AAU0379 standard; Protein; 298 AA.

AC AAU0379;
 DT 14-FEB-2002 (first entry)

DE Human adenine nucleotide translocator 2 (ANT2).

KM Human; adenine nucleotide translocator; ANT; ss;
 KM mitochondrial matrix protein.

OS Homo sapiens.

PN WO200185944-A2.

PD 15-NOV-2001.

PF 11-MAY-2001; 2001MO-US15416.

PR 11-MAY-2000; 2000US-0569327.

PA (MITO-) MITOKOR.

PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;
 PI Ghosh SS, Moos WH, Pei Y, Carroll AK;

DR MPI; 2002-055598/07.

DR N-PSDB; AAS16689.

PT Novel recombinant expression construct for producing adenine nucleotide
 PT translocator polypeptides, comprises a regulated promoter linked to
 PT nucleic acid encoding the polypeptide -
 PS Claim 44; Fig 2; 147pp; English.

CC The invention relates to a recombinant expression construct (I)
 CC comprising a regulated promoter operably linked to a nucleic acid
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
 CC culturing the host cell. (I) is also useful for targeting a polypeptide

CC of interest to a mitochondrial membrane, where ANT polypeptide is
 CC expressed as a fusion protein with the polypeptide of interest.
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT
 CC ligand is useful for determining the presence of an ANT polypeptide,
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
 CC ANT from a biological sample, where the ANT ligand is covalently or non-
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
 CC useful for identifying an agent that interacts with an ANT polypeptide.
 CC The present sequence represents the amino acid sequence of human ANT2.
 XX
 SQ Sequence 298 AA;
 Query Match 94.2%; Score 1454; DB 23; Length 298;
 Best Local Similarity 92.6%; Pred. No. 1.7e-147;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MTEQAISPAKDFLAGIAAIAISKTAVAPIERVKLLQVQHASKOIADKQYGIYDCIVR 60
 DB 1 MTDALSPAKDFLAGIAAIAISKTAVAPIERVKLLQVQHASKOIADKQYGIYDCIVR 60
 QY 61 IPKEGVLSFWRGNLANVIRFPPTQALNPAFOKTKQIFLGVDKHTQFMRYFAGNLASG 120
 DB 61 IPKEGVLSFWRGNLANVIRFPPTQALNPAFOKTKQIFLGVDKHTQFMRYFAGNLASG 120
 QY 121 GAAGATSLCFYVPLDPARTRLAADVSGSTERBERGLDCLVKTTSKGIRGLYQGFVS 180
 DB 121 GAAGATSLCFYVPLDPARTRLAADVSGSTERBERGLDCLVKTTSKGIRGLYQGFVS 180
 QY 181 VGGIIYYAAVFGYVDIAKGMLPDPKNTHTIVSWMIAQVTVAAGVSPDYVRRMM 240
 DB 181 VGGIIYYAAVFGYVDIAKGMLPDPKNTHTIVSWMIAQVTVAAGVSPDYVRRMM 240
 QY 241 OSGRGADIMTGTVDCKRKIRDBEGKAFKFGANSVLRGNGAFVLVDELK 296
 DB 241 OSGRGADIMTGTVDCKRKIRDBEGKAFKFGANSVLRGNGAFVLVDELK 296
 RESULT 10
 ABR41715
 ID ABR41715 standard; Protein; 429 AA.
 AC ABR41715;
 DT 02-JUN-2003 (first entry)
 DE Human DITHP organelle-associated protein.
 XX Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;
 XX cancer; cell proliferative disorder; autoimmune disorder;
 XX inflammatory disorder; infection; hormonal disorder; metabolic disorder;
 XX neurological disorder; gastrointestinal disorder; transport disorder;
 XX connective tissue disorder; drug screening; proteome analysis;
 XX gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
 XX disease model; toxicological testing; transcript imaging;
 XX organelle-associated protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200297031-A2.
 XX
 PD 05-DEC-2002.
 XX
 PF 27-MAR-2002; 2002WO-US10056.
 XX
 PR 28-MAR-2001; 2001US-279619P.
 PR 29-MAR-2001; 2001US-280067P.
 PR 29-MAR-2001; 2001US-280068P.
 PR 16-MAY-2001; 2001US-291280P.
 PR 17-MAY-2001; 2001US-291829P.
 PR 17-MAY-2001; 2001US-291849P.
 PR 19-JUN-2001; 2001US-299428P.
 PR 20-JUN-2001; 2001US-299776P.

PR 20-JUN-2001; 2001US-300001P.
 XX (INCY-) INCYTE GENOMICS INC.
 XX
 PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chlun J,
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amesley SR,
 PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleeefeld Y, Gerstin EH,
 PI Peraltas CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B,
 PI Flores V, Marwaha R, Lo A, Lan RX, Urashka ME;
 XX WPI; 2003-129518/12.
 DR N-PSDB; ACC46652.
 XX
 PT Novel human diagnostic and therapeutic polypeptide useful for
 PT identifying test compound which specifically binds to a polypeptide
 PT encoded by human diagnostic and therapeutic polynucleotide, and to
 PT induce antibodies -
 XX
 PS Claim 27; SEQ ID No 1250; 591pp; English.
 XX
 CC The invention relates to novel human diagnostic and therapeutic
 CC polynucleotides designated dithp (ACC46080-ACC46749) and to their
 CC encoded proteins (DITHP; ABR41136-ABR41812). The invention also relates
 CC to polynucleotide sequences at least 90% identical to the dithp cDNA
 CC sequences of the invention; recombinant vectors, host cells and
 CC transgenic organisms comprising a dithp nucleic acid sequence; the
 CC recombinant production of DITHP proteins; antibodies specific for DITHP
 CC proteins; microarrays comprising dithp nucleic acid sequences; methods
 CC of detecting dithp nucleotide and protein sequences; methods of screening
 CC for compounds which specifically bind a DITHP protein; and methods of
 CC assessing the toxicity of test compounds using a dithp hybridisation
 CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
 CC diagnosis of a wide variety of conditions including cancer and other cell
 CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,
 CC viral, fungal or parasitic infections; hormonal disorders; metabolic
 CC disorders; neurological disorders; gastrointestinal disorders; transport
 CC disorders; and connective tissue disorders. They may also be used to
 CC screen for modulators of protein activity or gene expression. DITHP
 CC proteins can additionally be used in analysis of the proteome of a tissue
 CC or cell type and to induce antibodies. The dithp nucleic acids are
 CC additionally useful in somatic or germline gene therapy of the disorders
 CC mentioned above, as a source of antisense sequences, as a source of
 CC probes and primers, in genotyping and identification of individuals, in
 CC the generation of transgenic animal models of human disease or knock in
 CC humanised animals, in toxicological testing, and in transcript imaging.
 CC The present sequence represents a DITHP protein which is an organelle-
 CC associated protein.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 429 AA;
 Query Match 91.9%; Score 1418; DB 24; Length 429;
 Best Local Similarity 95.2%; Pred. No. 2e-143;
 Matches 277; Conservative 3; Mismatches 5; Indels 6; Gaps 2;
 QY 1 MTEQAISPAKDFLAGIAAIAISKTAVAPIERVKLLQVQHASKOIADKQYGIYDCIVR 60
 DB 26 MTEQAISPAKDFLAGIAAIAISKTAVAPIERVKLLQVQHASKOIADKQYGIYDCIVR 85
 QY 61 IPKEGVLSFWRGNLANVIRFPPTQALNPAFOKTKQIFLGVDKHTQFMRYFAGNLASG 120
 DB 86 IPKEGVLSFWRGNLANVIRFPPTQALNPAFOKTKQIFLGVDKHTQFMRYFAGNLASG 145
 QY 121 GAAGATSLCFYVPLDPARTRLAADVSGSTERBERGLDCLVKTTSKGIRGLYQGFVS 180
 DB 146 GAAGATSLCFYVPLDPARTRLAADVSGSTERBERGLDCLVKTTSKGIRGLYQGFVS 205
 QY 181 VGGIIYYAAVFGYVDIAKGMLPDPKNTHTIVSWMIAQVTVAAGVSPDYVRRMM 240
 DB 206 VGGIIYYAAVFGYVDIAKGMLPDPKNTHTIVSWMIAQVTVAAGVSPDYVRRMM 265

QY 241 QSGRGADIMTGTVDGKRIKFRDEGKAFKGA-W-----SNVIRGKGA 285
 DB 266 QSGRGADIMTGTVDGKRIKFRDEGKAFKGA-FKGSWMKQATLADALEGSPSA 316

RESULT 11

AAW61169 standard; Protein; 298 AA.

AAW61169;

DT 28-SEP-1998 (first entry)

DE Anti protein.

Anti; Adenine nucleotide translocator; cloning; screening;
 DNA Tag diodeoxy terminator cycle sequencing; oxidative phosphorylation;
 probe; OXPHOS; mitochondria; ADP, ATP; homozygous mutant; myopathy;
 hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy;
 lactic acidosis; degenerative muscle disease.

OS Mus sp.

PN WO9819714-A1.

XX 14-MAY-1998.

PF 31-OCT-1997; 97WO-US19882.

PR 01-NOV-1996; 96US-0030017.

PA (UYEM-) UNIV EMORY.

PI Graham BC, Macgregor GR, Wallace DC;

DR WPI, 1998-286608/25.

DR N-PSDB; AAV36479.

PT Mice lacking heart-muscle adenine nucleotide translocator protein -
 useful as model for mitochondrial myopathy and hypertrophic
 cardiomyopathy in animals and to test therapeutic compositions or
 gene therapies

XX Disclosure; Page 39-40; 61pp; English.

PS The present sequence is the mouse Anti protein, the cDNA producing this
 CC polypeptide is cloned by screening a mouse heart cDNA library with the
 CC human Anti cDNA as a probe. The Anti cDNA sequence was determined by DNA
 CC Tag diodeoxy terminator cycle sequencing. The Anti protein is encoded by
 CC the Anti locus, a nuclear gene on chromosome 8. This protein is required
 CC in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP
 CC which can then be converted into ATP. An Anti homozygous mutant would
 CC thus be defective in OXPHOS which results in disease in oxidative
 CC metabolism dependent tissues. This mouse Anti homozygous mutant can be
 CC used as a model system for fascioscapular humeral muscular dystrophy,
 CC hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model
 CC systems can be used to test possible therapeutic compounds which
 CC increase/mediate ATP and ADP exchange across the mitochondrial membrane
 CC independent of ANT1.

XX Sequence 298 AA;

Query Match 91.5%; Score 1412; DB 19; Length 298;

Best Local Similarity 88.6%; Pred. No. 5.4e-143;

Matches 264; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEQAISPAKDFLAGGIAAISTKVAPIERVKLLQVQHASKOIADKQYGVDCIVR 60
 DB 1 MGDQALSTFLKDFLAGGIAAASKTAIVAPIERVKLLQVQHASKOISAEKQYGGIIDCVRR 60
 QY 61 IPKQGVLSFMRGNLANVIRYFPTQALNFAFDKXKQIFLGVDGHTQFWRYFAGNLASG 120
 DB 61 IPKQGVLSFMRGNLANVIRYFPTQALNFAFDKXKQIFLGVDGHTQFWRYFAGNLASG 120

QY 121 GAAGATSLCFYYPIDFAPTRLADVKSGETERERGLDCIVKTKSDGIRGLYQGESVS 180
 DB 121 GAAGATSLCFYYPIDFAPTRLADVKSGETERERGLDCIVKTKSDGIRGLYQGESVS 180

QY 181 VGGIITYAAAFYGYVDTAKGMLPDKNTHIVSNMIAQTVAVGVVSYPPTVARRMM 240
 DB 181 VGGIITYAAAFYGYVDTAKGMLPDKNTHIVSNMIAQTVAVGVVSYPPTVARRMM 240

QY 241 QSGRGADIMTGTVDGKRIKFRDEGKAFKGA-SNVLRGWGA-FVLVYDELKCVI 298
 DB 241 QSGRGADIMTGTVDGKRIKFRDEGKAFKGA-SNVLRGWGA-FVLVYDELKCVI 298

RESULT 12

ABUS3219

ID ABUS3219 standard; Protein; 293 AA.

XX ABUS3219;

AC ABUS3219;

DT 14-APR-2003 (first entry)

DE Human metabolism-associated DKFzpte3_35n12 homologue #1.

Human, gene therapy; vaccine, disease treatment; detection.

OS Homo sapiens.

PN WO200112659-A2.

XX 22-FEB-2001.

PF 18-AUG-2000; 2000WO-IB01496.

PR 18-AUG-1999; 99US-0149499.

PR 28-SEP-1999; 99US-0156503.

PA (GBHU-) GERMAN HUMAN GENOME PROJECT.

PI Wiemann S;

DR WPI, 2001-327840/34.

PT Nucleic acids having the sequences of clones isolated from libraries of
 different human tissues, useful in recombinant DNA methodologies -

XX Example III; Page 850; 1095pp; English.

PS This invention describes novel polynucleotides and polypeptides isolated
 CC from human cDNA libraries which can be used for gene therapy or in
 CC vaccines. The polynucleotides of the invention and antibodies encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate polypeptide expression. The products of the
 CC invention may also be used to identify modulators of expression and
 CC activity and to down regulate expression and activity. The antibodies of
 CC the invention may also be used as diagnostic agents for detecting the
 CC presence of polypeptides in samples. This sequence represents a homologue
 CC of a polypeptide described in the disclosure of the invention.

XX Sequence 293 AA;

Query Match 91.1%; Score 1406; DB 22; Length 293;

Best Local Similarity 90.1%; Pred. No. 2.3e-142;

Matches 263; Conservative 17; Mismatches 12; Indels 0; Gaps 0;

QY 5 AISPAPKDFLAGGIAAISTKVAPIERVKLLQVQHASKOIADKQYGVDCIVR 64
 DB 1 AISPAPKDFLAGGIAAISTKVAPIERVKLLQVQHASKOISAEKQYGGIIDCVRR 60
 QY 65 QGVLSFMRGNLANVIRYFPTQALNFAFDKXKQIFLGVDGHTQFWRYFAGNLASG 124
 DB 65 QGVLSFMRGNLANVIRYFPTQALNFAFDKXKQIFLGVDGHTQFWRYFAGNLASG 120

QY 125 ATSLCFVYPLDPFARTRLADVKGSGTEREFRGLADCLVKTSGDIRGLYOGFSVVGCI 184
 DB 121 ATSLCFVYPLDPFARTRLADVKGSGTEREFRGLADCLVKTSGDIRGLYOGFSVVGCI 180
 QY 185 IYRAAYGVYDTAKGMLPDPKNTTHIVVSMIAQTVAVAGVSYPEPTVRRMMQSGR 244
 DB 181 IYRAAYGVYDTAKGMLPDPKNTTHIVVSMIAQTVAVAGVSYPEPTVRRMMQSGR 240
 QY 245 KGADIMYGTVDCKWKIFRDEGSKAFPGKAMSVNLRMGGAFLVLYDELKVI 296
 DB 241 KGADIMYGTVDCKWKIFRDEGSKAFPGKAMSVNLRMGGAFLVLYDELKVI 292
 RESULT 13
 ID AA71031 standard; Protein; 297 AA.
 AC AA71031;
 XX 29-AUG-2000 (first entry)
 DE Human adenine nucleotide translocator ANTI.
 KW Human; adenine nucleotide translocator; ANTI; mitochondria; ADP; ATP;
 KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
 KW mitochondrial permeability transition; neuroprotective; neurotrophic;
 KW antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neurolytic;
 KW antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neurolytic;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dytonia;
 KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
 KW mitochondrial diabetes and deafness; hyperproliferative disorder;
 KW myoclonic epilepsy red ragged fibre syndrome.
 OS Homo sapiens.
 XX WO200026370-A2.
 PN 11-MAY-2000.
 PD 03-NOV-1999; 99WO-US25883.
 PF 03-NOV-1998; 98US-0185904.
 PR 08-SEP-1999; 99US-0393441.
 XX (MITO-) MITOKOR.
 PA Anderson CM, Davis RE, Clevenger W, Wiley SB, Miller SW, Szabo TR,
 PI Ghosh SS;
 DR WPI; 2000-365619/31.
 DR N-PSDB; AAD00519.
 XX Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease
 XX Claim 44; Page 172; 175pp; English.
 PS The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/citri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dytonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative

CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANTI from human brain.
 SQ Sequence 297 AA;
 Query Match 89.8%; Score 1385.5; DB 21; Length 297;
 Best Local Similarity 87.2%; Pred. No. 3.8e-140;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
 QY 1 MTEQALSPKADPLAGIAAISKTAIVAPIERVKLLLOVQASKOIADKQYKIVDCIVR 60
 DB 1 MGDHAWSEFLKDFLAGAVALAAVSKTAIVAPIERVKLLLOVQASKOIADKQYKIVDCIVR 60
 QY 61 IPKEQVLSFWRGLANVIRFPFOALNPAKDKYKQIFLGQVNHQFPMFYFGNLSAG 120
 DB 61 IPKEQVLSFWRGLANVIRFPFOALNPAKDKYKQIFLGQVNHQFPMFYFGNLSAG 120
 QY 121 GAAGTSLCFVYPLDPFARTRLADVKGSGTEREFRGLADCLVKTSGDIRGLYOGFSVS 180
 DB 121 GAAGTSLCFVYPLDPFARTRLADVKGSGTEREFRGLADCLVKTSGDIRGLYOGFSVS 179
 QY 181 VQGIITYRAAYGVYDTAKGMLPDPKNTTHIVVSMIAQTVAVAGVSYPEPTVRRMM 240
 DB 180 VQGIITYRAAYGVYDTAKGMLPDPKNTTHIVVSMIAQTVAVAGVSYPEPTVRRMM 239
 QY 241 QSGKADIMYGTVDCKWKIFRDEGSKAFPGKAMSVNLRMGGAFLVLYDELKVI 298
 DB 240 QSGKADIMYGTVDCKWKIFRDEGSKAFPGKAMSVNLRMGGAFLVLYDELKVI 297
 RESULT 14
 ID AAU01198 standard; Protein; 297 AA.
 AC AAU01198;
 XX 07-SEP-2001 (first entry)
 DE Human adenine nucleotide translocator-1 (ANT-1) protein.
 KW Human; adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 OS Homo sapiens.
 XX WO200132876-A2.
 PN 10-MAY-2001.
 PD 03-NOV-2000; 2000WO-US30535.
 PF 03-NOV-1999; 99US-043354.
 PR (MITO-) MITOKOR.
 PA Murphy AN, Clevenger W, Wiley SB, Andreyev AY, Fritger LG,
 PI Velicelcib G, Davis RE;
 DR WPI; 2001-291054/30.
 DR N-PSDB; AAS05901.
 XX New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX Disclosure; Fig 2; 186pp; English.
 PS The present sequence represents human adenine nucleotide translocator-1
 CC (ANT-1) protein. ANT proteins are mitochondrial permeability

CC transition (MTP) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transistion and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.

CC Sequence 297 AA;

Query Match 89.8%; Score 1385.5; DB 22; Length 297;

Best Local Similarity 87.2%; Pred. No. 3.8e-140;

Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTEQAISPAKDFLAGGIAAISKTAVAPIERVKLLQVQHASKQIAADKQYGIYDCIVR 60
 DB 1 MGDHMSFLKDFLAGAVALAAVSKTAVAPIERVKLLQVQHASKQISAEKQYGIIDCVVR 60
 QY 61 IPKEGVLSPFRGNLANVIRYPTQALNPAFKDKTKQIFLGVDVHKTFMRYFAGNLASG 120
 DB 61 IPKEGVLSPFRGNLANVIRYPTQALNPAFKDKTKQIFLGVDVHKTFMRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDPARTRLAADVGSKSTREBFGDGLVKTISDGINGLYQGFVS 180
 DB 121 GAAGATSLCFVYPLDPARTRLAADVGR-AQREHFGDGLVKTISDGLRGLYQGFVS 179
 QY 161 VGGIIYRAAYFGYVDTAKGMLPDPKNTHTIVSNMIAQVTAVAGVSPPTVRRMM 240
 DB 161 VGGIIYRAAYFGYVDTAKGMLPDPKNTHTIVSNMIAQSVTAVAGLSTPPTVRRMM 239
 QY 241 QSGRGADIMYTGTVDCMRKIFRDEGKAFKFGAMSNVLRMGCAFVLVYDELKQVI 298
 DB 240 QSGRGADIMYTGTVDCMRKIKADEGAKAFKFGAMSNVLRMGCAFVLVYDEIKQV 297

RESULT 15

AAU10378 standard; Protein; 297 AA.

XX AC AAU10378;
 XX DT 14-FEB-2002 (first entry)
 XX DE Human adenine nucleotide translocator 1 (ANT1).
 XX KW Human; adenine nucleotide translocator; ANT;
 XX KW mitochondrial matrix protein.
 XX OS Homo sapiens.
 XX PN WO200185944-A2.
 XX PD 15-NOV-2001.
 XX PF 11-MAY-2001; 2001WO-US15416.
 XX PR 11-MAY-2000; 2000US-0569327.
 XX PA (MITO-) MITOKOR.
 XX PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR,
 XX Ghosh SS, Moos WH, Pei Y, Carroll AK;

DR MPT; 2002-055598/07.
 DR N-PDB; AAS16688.

PT Novel recombinant expression construct for producing adenine nucleotide
 PT translocator polypeptides, comprises a regulated promoter linked to
 PT nucleic acid encoding the polypeptide

PS Claim 44, Fig 2, 147bp; English.

CC The invention relates to a recombinant expression construct (I)
 CC comprising a regulated promoter operably linked to a nucleic acid
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
 CC culturing the host cell. (I) is also useful for targeting a polypeptide
 CC of interest to a mitochondrial membrane, where ANT polypeptide is
 CC expressed as a fusion protein with the polypeptide of interest.
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT
 CC ligand is useful for determining the presence of an ANT polypeptide,
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
 CC ANT from a biological sample, where the ANT ligand is covalently or non-
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
 CC useful for identifying an agent that interacts with an ANT polypeptide.
 CC The present sequence represents the amino acid sequence of human ANT1.

CC Sequence 297 AA;

Query Match 89.8%; Score 1385.5; DB 23; Length 297;

Best Local Similarity 87.2%; Pred. No. 3.8e-140;

Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTEQAISPAKDFLAGGIAAISKTAVAPIERVKLLQVQHASKQIAADKQYGIYDCIVR 60
 DB 1 MGDHMSFLKDFLAGAVALAAVSKTAVAPIERVKLLQVQHASKQISAEKQYGIIDCVVR 60
 QY 61 IPKEGVLSPFRGNLANVIRYPTQALNPAFKDKTKQIFLGVDVHKTFMRYFAGNLASG 120
 DB 61 IPKEGVLSPFRGNLANVIRYPTQALNPAFKDKTKQIFLGVDVHKTFMRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDPARTRLAADVGSKSTREBFGDGLVKTISDGINGLYQGFVS 180
 DB 121 GAAGATSLCFVYPLDPARTRLAADVGR-AQREHFGDGLVKTISDGLRGLYQGFVS 179
 QY 161 VGGIIYRAAYFGYVDTAKGMLPDPKNTHTIVSNMIAQVTAVAGVSPPTVRRMM 240
 DB 161 VGGIIYRAAYFGYVDTAKGMLPDPKNTHTIVSNMIAQSVTAVAGLSTPPTVRRMM 239
 QY 241 QSGRGADIMYTGTVDCMRKIFRDEGKAFKFGAMSNVLRMGCAFVLVYDELKQVI 298
 DB 240 QSGRGADIMYTGTVDCMRKIKADEGAKAFKFGAMSNVLRMGCAFVLVYDEIKQV 297

Search completed: December 18, 2003, 12:40:47
 Job time : 36.3729 secs

RESULT 2
US-09-434-354-48
Sequence 48, Application US/09434354
Patent No. 6562563
GENERAL INFORMATION:
APPLICANT: Murphy, Anne N.
APPLICANT: Clevenger, William
APPLICANT: Wilev, Sandra Bileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Frigeri, Luciano G.
APPLICANT: Velicelab, Gonul
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
FILE REFERENCE: 660088.433
CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 48
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-434-354-48

Query Match 94.2%; Score 1454; DB 4; Length 298;
Best Local Similarity 92.6%; Pred. No. 5.2e-156;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEQASPAKDFLAGGIAAIAISKTAVAPIERVKLLQVQHSKQIAADKQYKGYVDCIVR 60
DB 1 MTDALSPAKDFLAGGIAAIAISKTAVAPIERVKLLQVQHSKQIADKQYKGYVDCIVR 60
QY 61 IPKCGVLSFMRGNLANVIRYPTQALNFAFKDKKQIFLGVDVGHQFMRYPAGNLASG 120
DB 61 IPKCBVLSFMRGNLANVIRYPTQALNFAFKDKKQIFLGVDVGHQFMRYPAGNLASG 120
QY 121 GAAGATSLCFYVPLDPFATRLAADVKGSGTEREFGDGLVKTSSDGIKGLYOGFSVS 180
DB 121 GAAGATSLCFYVPLDPFATRLAADVKGSGTEREFGDGLVKTSSDGIKGLYOGFSVS 180
QY 181 VGGIITRAAYFGVYDPAKGLPDPKNTIIVSNMIAQTVTAAGVSPEDTVRRMM 240
DB 181 VGGIITRAAYFGVYDPAKGLPDPKNTIIVSNMIAQTVTAAGVSPEDTVRRMM 240
QY 241 QSGRKGADIMVTGTLDCKRKIADEGGAFFKGAWSNVLKMGAFVLVLYDEIKK 296
DB 241 QSGRKGADIMVTGTLDCKRKIADEGGAFFKGAWSNVLKMGAFVLVLYDEIKK 296

RESULT 3

US-08-961-871-10
Sequence 10, Application US/08961871
Patent No. 6013858
GENERAL INFORMATION:
APPLICANT: Wallace, Douglas C.
APPLICANT: Graham, Brett H.
APPLICANT: MacGregor, Grant R.
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Reiber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-961-871-10

Query Match 91.5%; Score 1412; DB 3; Length 298;
Best Local Similarity 88.6%; Pred. No. 2.9e-151;
Matches 264; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEQASPAKDFLAGGIAAIAISKTAVAPIERVKLLQVQHSKQIAADKQYKGYVDCIVR 60
DB 1 MTDALSPAKDFLAGGIAAIAISKTAVAPIERVKLLQVQHSKQIADKQYKGYVDCIVR 60
QY 61 IPKCGVLSFMRGNLANVIRYPTQALNFAFKDKKQIFLGVDVGHQFMRYPAGNLASG 120
DB 61 IPKCBVLSFMRGNLANVIRYPTQALNFAFKDKKQIFLGVDVGHQFMRYPAGNLASG 120
QY 121 GAAGATSLCFYVPLDPFATRLAADVKGSGTEREFGDGLVKTSSDGIKGLYOGFSVS 180
DB 121 GAAGATSLCFYVPLDPFATRLAADVKGSGTEREFGDGLVKTSSDGIKGLYOGFSVS 180
QY 181 VGGIITRAAYFGVYDPAKGLPDPKNTIIVSNMIAQTVTAAGVSPEDTVRRMM 240
DB 181 VGGIITRAAYFGVYDPAKGLPDPKNTIIVSNMIAQTVTAAGVSPEDTVRRMM 240
QY 241 QSGRKGADIMVTGTLDCKRKIADEGGAFFKGAWSNVLKMGAFVLVLYDEIKK 298
DB 241 QSGRKGADIMVTGTLDCKRKIADEGGAFFKGAWSNVLKMGAFVLVLYDEIKK 298

RESULT 4

US-09-434-354-47
Sequence 47, Application US/09434354
Patent No. 6562563
GENERAL INFORMATION:
APPLICANT: Murphy, Anne N.
APPLICANT: Clevenger, William
APPLICANT: Wilev, Sandra Bileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Frigeri, Luciano G.
APPLICANT: Velicelab, Gonul
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
FILE REFERENCE: 660088.433
CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 47
LENGTH: 297
TYPE: PRT
ORGANISM: Homo sapien

US-09-434-354-47

Query Match 89.8%; Score 1385.5; DB 4; Length 297;
Best Local Similarity 87.2%; Pred. No. 2,9e-148;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTEQALISAKPDLIAGIAAIAISKTVAPLIERKLLIQVHASKQJADKQYGIYDVCYR 60
DB 1 MODHMSLKLQPLAAGVAAVAASKTAVAPLERKLLIQVHASKQJADKQYGIYDVCYR 60
QY 61 IPKEQGLSPWNGNLANVIRYPTQALNPAFQKXKQJIFLQGVDRKHTQFWRYPAGNLASG 120
DB 61 IPKEQGLSPWNGNLANVIRYPTQALNPAFQKXKQJIFLQGVDRKHTQFWRYPAGNLASG 120
QY 121 GAAGTSLCFVYPLDPAFTRIAADYKSGTEREPFGDLCLVTKTSQIGRLYQGSFVS 180
DB 121 GAAGTSLCFVYPLDPAFTRIAADYKSGTEREPFGDLCLVTKTSQIGRLYQGSFVS 180
QY 181 VQGIITPAAVYGVYDTAKGMLPDPKNTHTIVSNMIAQTVAVAGVSVYPTVRRMM 240
DB 180 VQGIITPAAVYGVYDTAKGMLPDPKNTHTIVSNMIAQTVAVAGVSVYPTVRRMM 240
QY 241 QSGRRGADIMYTGVDCKRKIFRDEGKAFKFGANSVLRGNGGAFVLVLYDELKXVI 298
DB 240 QSGRRGADIMYTGVDCKRKIAKDEGAKAFKFGANSVLRGNGGAFVLVLYDEIKXV 297

RESULT 5
US-09-996-243-289
Sequence 289, Application US/09996243
Patent No. 6478825

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Auecin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P13
CURRENT APPLICATION NUMBER: US/09/996,243
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598

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      PRIOR APPLICATION NUMBER: 60/091626
      PRIOR FILING DATE: 1998-07-02
      PRIOR APPLICATION NUMBER: 60/091633
      PRIOR FILING DATE: 1998-07-02
      PRIOR APPLICATION NUMBER: 60/091978
      PRIOR FILING DATE: 1998-07-07
      PRIOR APPLICATION NUMBER: 60/091982
      PRIOR FILING DATE: 1998-07-07
      PRIOR APPLICATION NUMBER: 60/092182
      PRIOR FILING DATE: 1998-07-09

Query Match          20.3%; Score 314; DB 4; Length 469;
Beet Local Similarity 30.1%; Pred. No. 7.8e-27;
Matches 89; Conservative 60; Mismatches 115; Indels 32; Gaps 11;

Oy 10 KDLFAGGIAAISTKTAAPIERVKLLIQVQHASKQIADKQYGIYDCIVRIPEOGVLS 69
    :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 188 RHLVAGGGAGAVSRTCAPIRLKVLNQV-HASR-----SNMNGIVGGFTQMIREGAR 241
    ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Oy 70 FWRGNLANVIRYPEPTQALNFAFDKTKQKQIFLGGVDKHGTQFWRYPAUGNLASGAAGATSLC 129
    ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 242 LMRNGINLVKLIAESAIKFMAVEQIKR--LVGSDBET---LRHIEPLVAGSLAGAIAOS 296
    ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Oy 130 FYVLEDPARTRILADVKSGETEREFRGLDCLVTXITSDGIRIGLYOGFSVSVOGIIYYRA 189
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 297 SIYMELVLRKRM--LKRG---QYSMDLCARRILARBVAAFYKYGVNMGLIIFYAG 351
    ::||::||::||::||::||::||::||::||::||::||::||::||::||
Oy 190 AYFGVDYTDAKM-----LPDEKNTHIVSMNIACVTAAVAG-VVSYPPDYRRRMM 240
    ||::||::||::||::||::||::||::||::||::||::||::||::||
Db 352 IDLAIVEFLKNAMQLQHYAVNSADPG---VFVLLACGTMSTCGQLASYPLALVTRMOA 407
    ||::||::||::||::||::||::||::||::||::||::||::||::||
Oy 241 QSGEKADIMYTGVDCWKRIFRDEGKAFFPKGAMSIVLAGMGAPV-LVIYDELK 295
    |:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 408 QASIEGAEVMTSSL-FKHILTEGAFGLYRGLAFPMKVIPAIVASISYVENLK 461
    ::||::||::||::||::||::||::||::||::||::||::||::||::||

RESULT 6
US-09-188-930-339
Sequence 339; Application US/09188930A
Patent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorina
APPLICANT: Sleeman, Matthew
APPLICANT: Ontust, Rene
APPLICANT: Muirson, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
FILE REFERENCE: 11009.101ic1
CURRENT APPLICATION NUMBER: US/09/188.930A
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 339
LENGTH: 469
TYPES: PRT
ORGANISM: Mouse
US-09-188-930-339

Query Match          20.2%; Score 311; DB 3; Length 469;
Beet Local Similarity 29.4%; Pred. No. 1.7e-26;
Matches 88; Conservative 62; Mismatches 111; Indels 38; Gaps 11;

Oy 10 KDPLAGGIAAISKTAAPIERVKLLIQVQHASKQIADKQYGIYDCIVRIPEOGVLS 69
    :|::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 188 RHLVAGGGAGAVSRTCAPIRLKVLNQV-HASR-----SNMNCIYGFTQMIREGAR 241
    ||::||::||::||::||::||::||::||::||::||::||::||::||
Oy 70 FWRGNLANVIRYPEPTQALNFAFDKTKQKQIFLGGVDKHGTQFWRYPAUGNLASGAAGATSLC 129
    ||||::||::||::||::||::||::||::||::||::||::||::||::||
Db 242 LMRNGINLVKLIAESAIKFMAVEQIKR--LVGSDBET---LRHIELVAGSLAGAIAOS 296
    ||::||::||::||::||::||::||::||::||::||::||::||::||
Oy 130 FYVLEDPARTRILADVKSGETEREFRGLDCLVKITKSDGIRLQYGFVSVOGIIYYRA 189
    :|::||::||::||::||::||::||::||::||::||::||::||::||

```

Db 297 SIYMEVLTAKTMA--LRKTG---QYSGMLDCARRILAKESGAAPYKGIYPMNLGIIPYAG 351
 QY 190 AYFGYDTAKGMLDPKXKTHI-----VYSMMIAQTVTVAG--VVSYPDTYRRR 237
 Db 352 IDLAVETL-----KXWLORYAVNSADGCVFLACGTTISCTCGGLASYPPLAVRTR 404
 QY 238 MMQSGRGKADIMYTGTVDCWRKIFRDEGKAFKFGKMSNYLRGKGAFV-LVLYDELX 295
 Db 405 MQAQSIEGAPEVTMSSL--FKQILRTGAGFGLYRGLAPNPKVIYPAVISIYVYENLK 461

RESULT 7

US-09-312-283C-339
 ; Sequence 339, Application US/09312283C
 ; Patent No. 6573095
 ; GENERAL INFORMATION:

; APPLICANT: Watson, James D.
 ; APPLICANT: Strachan, Lorna
 ; APPLICANT: Sleeman, Matthew
 ; APPLICANT: Onrust, Rene
 ; APPLICANT: Murison, James G.
 ; APPLICANT: Kumble, Krishanand D.
 ; TITLE OF INVENTION: Compositions Isolated from Skin Cells
 ; TITLE OF INVENTION: and Methods for Their Use
 ; FILE REFERENCE: 11000.1011C2
 ; CURRENT APPLICATION NUMBER: US/09/312,283C
 ; CURRENT FILING DATE: 1999-05-14
 ; NUMBER OF SEQ ID NOS: 425
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 339
 ; LENGTH: 469
 ; TYPE: PRT
 ; ORGANISM: Mouse
 ; US-09-312-283C-339

Query Match 20.2%; Score 311; DB 4; Length 469;
 Best Local Similarity 29.4%; Pred. No. 1.7e-26;
 Matches 86; Conservative 62; Mismatches 111; Indels 38; Gaps 11;

QY 10 KDLPLAGGIAAISTKTAAPIERVKLLIQVQHAS--KQIADKQYKGIYDCIVRIPIK 69
 Db 188 RHLVAGGAGAVSRTCTAPDLRLKVMQV--HASS-----SNMNCIVGGFTMIREGAKS 241
 QY 70 FWRGNLANVIRFPFOALNFAFKDKYKQIFLGGVDKHQFWRYPFAGNLSGGAAGATSLC 129
 Db 242 LMRGNGINVLKIAESAIKFAAYEQMR--LVGSDQET--LRHERLVASGLAGALAQ 296
 QY 130 FVYPLDPAFRTLADVQSGTEREFGLDCLVKTISDGRGHYQGSFVSVOGI1IYRA 189
 Db 297 SIYMEVLTAKTMA--LRKTG---QYSGMLDCARRILAKESGAAPYKGIYPMNLGIIPYAG 351
 QY 190 AYFGYDTAKGMLDPKXKTHI-----VYSMMIAQTVTVAG--VVSYPDTYRRR 237
 Db 352 IDLAVETL-----KXWLORYAVNSADGCVFLACGTTISCTCGGLASYPPLAVRTR 404
 QY 238 MMQSGRGKADIMYTGTVDCWRKIFRDEGKAFKFGKMSNYLRGKGAFV-LVLYDELX 295
 Db 405 MQAQSIEGAPEVTMSSL--FKQILRTGAGFGLYRGLAPNPKVIYPAVISIYVYENLK 461

RESULT 8

US-09-482-273-118
 ; Sequence 118, Application US/09482273
 ; Patent No. 6534631
 ; GENERAL INFORMATION:

; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 71 Human Secreted Proteins
 ; FILE REFERENCE: P2030B1
 ; CURRENT APPLICATION NUMBER: US/09/482,273
 ; CURRENT FILING DATE: 2000-01-13
 ; EARLIER APPLICATION NUMBER: PCT/US99/15849
 ; EARLIER FILING DATE: 1999-07-14
 ; EARLIER APPLICATION NUMBER: 60/092,921

; EARLIER FILING DATE: 1998-07-15
 ; EARLIER APPLICATION NUMBER: 60/092,922
 ; EARLIER FILING DATE: 1998-07-15
 ; EARLIER APPLICATION NUMBER: 60/092,956
 ; EARLIER FILING DATE: 1998-07-15
 ; NUMBER OF SEQ ID NOS: 267
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 118
 ; LENGTH: 335
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (335)
 ; OTHER INFORMATION: (335)
 ; US-09-482-273-118

Query Match 18.5%; Score 286; DB 4; Length 335;
 Best Local Similarity 29.0%; Pred. No. 6.9e-24;
 Matches 87; Conservative 50; Mismatches 133; Indels 30; Gaps 8;

QY 10 KDLPLAGGIAAISTKTAAPIERVKLLIQVQHAS--KQIADKQYKGIYDCIVRIPIK 64
 Db 51 KPEVYGGIASIVAFEGTFPVDLTETRLQVQGSIDARFKEI---KTRGMFHALFRICKE 106
 QY 65 QGVLSFRGNLANVIRFPFOALNFAFKDKYKQIFLGGVDKHQFWRYPFAGNLSGGAAG 124
 Db 107 EGVLAISGIAAPLARKASGTGKIGIYQSLKRLVERLDET-----LLINMGVAVSG 161
 QY 125 ATSLCFYPLDPAFRTLADVQSGTEREFGLDCLVKTISDGRGHYQGSFVSVOGI 184
 Db 162 VISSTIANPVDVLRKIRQA-----QGLFQSGMIGS-FIDYQSGCTGRLRGVPTPQRA 216
 QY 185 IYRAAYGYDTAK-----GMLDPKXKTHIYVSMIAQTVTVAGVSYPTYRRR 238
 Db 217 AIVGVGLPVDITKRLILSGMMGDTILTFVVSF-----TCGLAGALASNPVDVVRTRM 272
 QY 239 MMQSGRGKADIMYTGTVDCWRKIFRDEGKAFKFGKMSNYLRGKGAFV-LVLYDELX 297
 Db 273 MNQRAIVGHVDLTKGIVDGILKMKHKGFPALYKGFPMNLRLGPNNIIFPITYEQLRL 332

RESULT 9

US-09-501-558-2
 ; Sequence 2, Application US/09501558
 ; Patent No. 6403784
 ; GENERAL INFORMATION:

; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Mathur, Brian
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: No. 6403784e1 Human Uncoupling Proteins and
 ; FILE REFERENCE: LEX-0012-USA
 ; CURRENT APPLICATION NUMBER: US/09/501,558
 ; CURRENT FILING DATE: 2000-02-09
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 291
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-501-558-2

Query Match 18.4%; Score 283.5; DB 4; Length 291;
 Best Local Similarity 28.9%; Pred. No. 1.1e-23;
 Matches 87; Conservative 54; Mismatches 129; Indels 31; Gaps 9;

QY 10 KDLPLAGGIAAISTKTAAPIERVKLLIQVQHAS--KQIADKQYKGIYDCIVRIPIK 64
 Db 7 KPEVYGGIASITAECCGTFPDLTKETRLQVQGSIDARFKEI---RYRGMHLVLRIGRE 62
 QY 65 QGVLSFRGNLANVIRFPFOALNFAFKDKYKQIFLGGVDKHQFWRYPFAGNLSGGAAG 124

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Db      63 EQLKLYSGIAPAMLRQASVGTIKIGTQSLRLRLTERPEDET-----LPINVICGISG 117
Qy      125 ATSLCFVPLDPAFTRILADVKGSTEREFRLGDLVITKSDGIRGLYQGFVSVOGI 184
Db      118 VISSIANPTDVLKIRMOA-----QSNITIQ--GGMINFNMIYQGBETRLGMKVSILTAQRA 172
Qy      185 IIRAYVGVYDTAK-----GMLDPPKXTHIVSMMIAQTVTAAGVVSYPFDVRRM 238
Db      173 AIVVGVLPVYDITKKHLILSGIMGDDVYTHFLSSF-----TCGLAGALASNPVDVVRTRM 228
Qy      239 MMQSG-RKGADIMYGTVDGCMRKIFRDGSGKAFPFKAGMSNVLR--GMGAFLVLYLDELTK 296
Db      229 MNQVLRDGRSGYGTITDCLLQTKMKGFFALYKGFWMNLRLLPMMIIFVYEQULK 288
Qy      297 V 297
Db      289 L 289
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RESULT 10
US-09-160-119-4
; Sequence 4, Application US/09160119A
; Patent No. 6316219
; GENERAL INFORMATION:
; APPLICANT: KRIEF, STEPHANE
; APPLICANT: SOUCHEM, MICHEL
; APPLICANT: BRILL, ANTOINE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30985
; CURRENT APPLICATION NUMBER: US/09/160,119A
; CURRENT FILING DATE: 1998-09-24
; EARLIER APPLICATION NUMBER: EP 97402511.6
; EARLIER FILING DATE: 1997-10-23
; EARLIER APPLICATION NUMBER: EP 98401655.0
; EARLIER FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 447
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-160-119-4
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Query Match      18.1%; Score 280; DB 4; Length 447;
Best Local Similarity 27.1%; Pred. No. 5.1e-23;
Matches 80; Conservative 47; Mismatches 148; Indels 20; Gaps 6;

Qy      4 QAIAPKADFLAGGIAAISTKNAVAPIERYKLLQVQHASKOIADKQYKGIYDCLVRIPK 63
Db      96 QVABSAVRFGLGSVAGAVATAVPIIDVKTMOQRSTGSFVGLMVKNSPDCPKVLR 155
Qy      64 EOGVLSFWRGMLANVIRFPTQALNFAFKDKYKQIPL---GGVDKHTQFWRYFAGNLSAG 120
Db      156 YEGFGLYRGLLPOLLGVAPEKAIKLTYNDFPRDKFMKQSVP-----LAAELIAG 207
Qy      121 GAAGATSLCFVYPLDPAFTRILADVKGSTEREFRLGDLVITKSDGIRGLYQGFVS 180
Db      208 GCAGSGVITFTNPLIIVKIRLQV--AGEITTGPRVSAL-----SVVRDGLGFGIYKGAAC 261
Qy      181 VQGIITRYAAVFGVYDTRAKGMLPDPKXTHIVSMMIAQTVTA--AGVVSYPFDVRRM 239
Db      262 FLRDIPEAIYFPCYAHVYKASFPANEDQVSPGSLILAGAIQMPAASLVTPADVYKTR-- 319
Qy      240 MOSGRKADIMYGTVDGCMRKIFRDGSGKAFPFKAGMSNVLRGMGAFLVLYDEL 294
Db      320 LQVAPRAQGTYSVVIDCFRKILREBGRKALMKAGARVFRSSPQGVYTLTYEL 374
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RESULT 11
US-09-160-119-2
; Sequence 2, Application US/09160119A
; Patent No. 6316219
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; GENERAL INFORMATION:
; APPLICANT: KRIEF, STEPHANE
; APPLICANT: SOUCHEM, MICHEL
; APPLICANT: BRILL, ANTOINE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30985
; CURRENT APPLICATION NUMBER: US/09/160,119A
; CURRENT FILING DATE: 1998-09-24
; EARLIER APPLICATION NUMBER: EP 97402511.6
; EARLIER FILING DATE: 1997-10-23
; EARLIER APPLICATION NUMBER: EP 98401655.0
; EARLIER FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 674
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-160-119-2
```

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Query Match      18.1%; Score 280; DB 4; Length 674;
Best Local Similarity 27.1%; Pred. No. 9.4e-23;
Matches 80; Conservative 47; Mismatches 148; Indels 20; Gaps 6;

Qy      4 QAIAPKADFLAGGIAAISTKNAVAPIERYKLLQVQHASKOIADKQYKGIYDCLVRIPK 63
Db      323 QVABSAVRFGLGSVAGAVATAVPIIDVKTMOQRSTGSFVGLMVKNSPDCPKVLR 382
Qy      64 EOGVLSFWRGMLANVIRFPTQALNFAFKDKYKQIPL---GGVDKHTQFWRYFAGNLSAG 120
Db      383 YEGFGLYRGLLPOLLGVAPEKAIKLTYNDFVRDKFMKQSVP-----LAAELIAG 434
Qy      121 GAAGATSLCFVYPLDPAFTRILADVKGSTEREFRLGDLVITKSDGIRGLYQGFVS 180
Db      435 GCAGSGVITFTNPLIIVKIRLQV--AGEITTGPRVSAL-----SVVRDGLGFGIYKGAAC 488
Qy      181 VQGIITRYAAVFGVYDTRAKGMLPDPKXTHIVSMMIAQTVTA--AGVVSYPFDVRRM 239
Db      489 FLRDIPEAIYFPCYAHVYKASFPANEDQVSPGSLILAGAIQMPAASLVTPADVYKTR-- 546
Qy      240 MOSGRKADIMYGTVDGCMRKIFRDGSGKAFPFKAGMSNVLRGMGAFLVLYDEL 294
Db      547 LQVAPRAQGTYSVVIDCFRKILREBGRKALMKAGARVFRSSPQGVYTLTYEL 601
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RESULT 12
US-09-142-565-2
; Sequence 2, Application US/09142565A
; Patent No. 6187560
; GENERAL INFORMATION:
; APPLICANT: Lee James Beeley
; APPLICANT: Kelly Paine
; APPLICANT: Robert James
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30002
; CURRENT APPLICATION NUMBER: US/09/142,565A
; CURRENT FILING DATE: 1999-06-30
; EARLIER APPLICATION NUMBER: 9704551.2
; EARLIER FILING DATE: 1997-03-05
; EARLIER APPLICATION NUMBER: 9705614.7
; EARLIER FILING DATE: 1997-03-18
; EARLIER APPLICATION NUMBER: 97305305.1
; EARLIER FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
US-09-142-565-2
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Query Match      17.2%; Score 265; DB 3; Length 312;
Best Local Similarity 27.1%; Pred. No. 1.5e-21;
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Matches      82; Conservative      52; Mismatches      145; Indels      24; Gaps      8

QY      7 SPADFLAGGIAAIAISKTAAPIERKYLLOVQ--HASKQIADQKYKIVDCIYRIPEK 64
DB      12 TMAVVEFLAGTAACPADIVTPELDDAKYRLQIOGENOAQVTA RLQVYGVGLTITLWRT 71
QY      65 QGVLSFMKGNLANVRYEPTQALNPAFKDKYQIFL-GGVDDHGTQFWRYFAGNLASGGA 123
DB      72 EGPSPYNGLVAGLQKQMSFASIRIGLYDSVQVTPPKADSSLTTLA----GCTT 126
QY      124 GATSLCFYPLDPFATRLAADY--GKSGTEREFRGLGDLVXITSDGIRGLYOGFSVSU 181
DB      127 GAMATCAQPDIVVAVRFQASIHLDSPNSDRKTSCTMDAYRTIAEBGVKGMKTLXNI 186
QY      182 QGIIITRAAYFEGVDTPAKGMLPDPKXTHIVSMMLAQVTYA----VAGVSYSPDVTAR 236
DB      187 MRNAIVNCAEVVTYDILKEKLID---YHLLTNPCHFSAPGAGFACATVVASPDVYKT 243
QY      237 RMMMGSGKRGADIMTGTGVDCRRIKFRBGCGAPFKGMSNLR-GMGAPLVLYYDELK 295
DB      244 RYM-----NSPPGQYFSPIDCMIKNAQDEGPTAFYKGFPTSPRLGSMNVVAFVTEOLK 298
QY      296 KVI 298
DB      299 RAL 301

RESULT 13
US-08-518-878B-56
; Sequence 56, Application US/08518878B
; Patent No. 5702902.
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U S A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/518,878B
; FILING DATE: 23-AUG-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 299 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; US-08-518-878B-56

Query Match      16.2%; Score 250.5; DB 1; Length 299;
Best Local Similarity 24.9%; Pred. No. 66-20;
Matches      74; Conservative      52; Mismatches      146; Indels      25; Gaps      8

12 FLAGGIAAIAISKTAAPIERVTLIIQVQHAK--QIADQKYKIVDCIYRIPEKGLV 68

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QY 129 CFVYLDPAFTPLADVGKSGTEREFGCLVITTSDDIRGLYQGSVSVOGIIYR 188
DB 122 AVAQPTDVVKYFQAQ-ARAGGRRYQSVNNAKYKTIAREEGFRGLMKGSPVANAALVN 180
QY 169 AAYFVYDPAK-----GMLPDPKNTHTVSWMIAQTVAVAGVSVYPDTVRRMMQMS 242
DB 181 CAELVYTDLIKALKANIMTDDLPCHFTSARAGFCITVIAAS---PVDVVKTRYM--- 233
QY 243 GRKGADIMYGTVDWCWKIFRDEGGKAFPKGAMSNVLR-GMGAFVLVLYDELKKVI 298
DB 234 --NSALGGYSSAGHCALTMLQKEGPRAFYKGFMPSPFLRGSWNVVMFVYEQDKRAL 288

RESULT 15
US-08-518-878B-51
; Sequence 51, Application US/08518878B
; Patent No. 5702902

GENERAL INFORMATION:
; APPLICANT: Tartaglie, Louis A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/518,878B
; FILING DATE: 23-AUG-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELETEXT: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; US-08-518-878B-51

Query Match 16.2%; Score 250.5; DB 1; Length 309;

Best Local Similarity 24.9%; Pred. No. 6.3e-20;

Matches 74; Conservative 52; Mismatches 146; Indels 25; Gaps 8;

QY 12 FLAGGIAAISTKNAVPIERVLLLOVOHASK---QIADKQYKGIIVDCIIVIRPKQGV 68
DB 17 FLGACTAACIADLITFPLDTAKVRLQIGESQGPVATVSAQYKGMGTILTMVTEGPR 76
QY 69 SEWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLAGGAAGATSL 128
DB 77 SLVNGLVAGLQROMSPASVRIGLYDSVKQFYTKG-SEHAS-----IGSRLLAGSTGALAV 131
QY 129 CFVYLDPAFTPLADVGKSGTEREFGCLVITTSDDIRGLYQGSVSVOGIIYR 188
DB 132 AVAQPTDVVKYFQAQ-ARAGGRRYQSVNNAKYKTIAREEGFRGLMKGSPVANAALVN 190
QY 189 AAYFVYDPAK-----GMLPDPKNTHTVSWMIAQTVAVAGVSVYPDTVRRMMQMS 242
DB 191 CAELVYTDLIKALKANIMTDDLPCHFTSARAGFCITVIAAS---PVDVVKTRYM--- 243

QY 243 GRKGADIMYGTVDWCWKIFRDEGGKAFPKGAMSNVLR-GMGAFVLVLYDELKKVI 298
DB 244 --NSALGGYSSAGHCALTMLQKEGPRAFYKGFMPSPFLRGSWNVVMFVYEQDKRAL 298

Search completed: December 18, 2003, 12:44:56
Job time: 13.3471 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:43:17 ; Search time 24.3606 Seconds
(without alignments)
2284.595 Million cell updates/sec

Title: US-09-811-131-33
Perfect score: 1543
Sequence: 1 MTEQALSFADFLAGGIAA.....LRGKGAFLVLYDELKKVI 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*
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11: /cgn2_6/ptodata/2/pubppa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1543	100.0	298	9 US-09-811-094-33	Sequence 33, Appl
2	1543	100.0	298	9 US-09-810-644-33	Sequence 33, Appl
3	1543	100.0	298	10 US-09-185-804A-33	Sequence 33, Appl
4	1454	94.2	298	9 US-09-811-094-32	Sequence 32, Appl
5	1454	94.2	298	9 US-09-810-644-32	Sequence 32, Appl
6	1454	94.2	298	10 US-09-185-804A-32	Sequence 32, Appl
7	1385.5	89.8	297	9 US-09-811-094-31	Sequence 31, Appl
8	1385.5	89.8	297	9 US-09-810-644-31	Sequence 31, Appl
9	1385.5	89.8	297	10 US-09-185-804A-31	Sequence 31, Appl
10	811	52.6	179	12 US-10-032-386-32501	Sequence 32501, A
11	788.5	51.1	301	12 US-10-032-386-32501	Sequence 7194, Ap
12	760.5	49.3	318	10 US-09-801-368-252	Sequence 252, App
13	749.5	48.6	386	9 US-09-734-569-170	Sequence 170, App
14	737	47.8	308	15 US-10-128-714-3338	Sequence 3338, Ap
15	737	47.8	308	15 US-10-128-714-8338	Sequence 8338, Ap

16	734.5	47.6	381	12 US-10-141-478A-2	Sequence 2, Appl
17	686	44.5	677	12 US-10-259-165-192	Sequence 192, App
18	518	33.6	132	9 US-09-925-101-1459	Sequence 1459, App
19	423	27.4	87	9 US-09-864-761-36440	Sequence 36440, A
20	368	23.8	475	10 US-09-777-921A-4	Sequence 4, Appl
21	368	23.8	477	10 US-09-777-921A-2	Sequence 2, Appl
22	333.5	21.6	410	10 US-09-777-921A-5	Sequence 5, Appl
23	336	21.1	384	12 US-10-094-749-1789	Sequence 1789, Ap
24	314	20.3	469	9 US-09-989-722-289	Sequence 289, App
25	314	20.3	469	9 US-09-989-723-289	Sequence 289, App
26	314	20.3	469	9 US-09-989-729-289	Sequence 289, App
27	314	20.3	469	9 US-09-989-727-289	Sequence 289, App
28	314	20.3	469	10 US-09-989-731-289	Sequence 289, App
29	314	20.3	469	10 US-09-989-732-289	Sequence 289, App
30	314	20.3	469	10 US-09-991-073-289	Sequence 289, App
31	314	20.3	469	10 US-09-990-442-289	Sequence 289, App
32	314	20.3	469	10 US-09-991-163-289	Sequence 289, App
33	314	20.3	469	10 US-09-993-604-289	Sequence 289, App
34	314	20.3	469	10 US-09-990-456-289	Sequence 289, App
35	314	20.3	469	10 US-09-989-721-289	Sequence 289, App
36	314	20.3	469	10 US-09-992-598-289	Sequence 289, App
37	314	20.3	469	10 US-09-989-293A-289	Sequence 289, App
38	314	20.3	469	10 US-09-989-735-289	Sequence 289, App
39	314	20.3	469	10 US-09-990-444-289	Sequence 289, App
40	314	20.3	469	10 US-09-991-181-289	Sequence 289, App
41	314	20.3	469	10 US-09-989-730-289	Sequence 289, App
42	314	20.3	469	10 US-09-990-436-289	Sequence 289, App
43	314	20.3	469	10 US-09-993-687-289	Sequence 289, App
44	314	20.3	469	11 US-09-989-734-289	Sequence 289, App
45	314	20.3	469	11 US-09-997-653-289	Sequence 289, App

ALIGNMENTS

RESULT 1
US-09-811-094-33
Sequence 33, Application US/09811094
Patent No. US2001004144A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
FILE REFERENCE: 660088.420D4
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-811-094-33
Query Match 100.0%; Score 1543; DB 9; Length 298;
Best Local Similarity 100.0%; Pred. No. 1e-156;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTEQALSFADFLAGGIAAISTKTAVERVLLQVQASAKQIADKQYGVDCIVR 60
DB 1 MTEQALSFADFLAGGIAAISTKTAVERVLLQVQASAKQIADKQYGVDCIVR 60
QY 61 IPKEQGLTSEWRGNLANVIRYPTQALNFAFKQYKQIFLGVDKHTQFRYFAGNLASG 120
DB 61 IPKEQGLTSEWRGNLANVIRYPTQALNFAFKQYKQIFLGVDKHTQFRYFAGNLASG 120

Qy 121 GAAGATSLCFYPPDLPARTLAADVKGSGTEREFGDCLVKTSGIKGLYOGFSVS 180
Db 121 GAAGATSLCFYPPDLPARTLAADVKGSGTEREFGDCLVKTSGIKGLYOGFSVS 180
Qy 181 VGGIITRAAFYGVYDTAKGMLPDPKNTHTIVSWMIAGTVAVAGVSYPPDYARRMM 240
Db 181 VGGIITRAAFYGVYDTAKGMLPDPKNTHTIVSWMIAGTVAVAGVSYPPDYARRMM 240
Qy 241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFFKGAMSNVLRMGGAFLVLYDELKVI 238
Db 241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFFKGAMSNVLRMGGAFLVLYDELKVI 238

RESULT 2
US-09-810-644-33

Sequence 33, Application US/09810644
Patent No. US20020012992A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pel, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D3
CURRENT APPLICATION NUMBER: US/09/810.644
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-810-644-33

Query Match 100.0%; Score 1543; DB 9; Length 298;
Best Local Similarity 100.0%; Pred. No. 1e-156;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTEQAISFADFLAGIAAISTAVAPIERVKLLQVQHASKOIADKQYKGIIVDCIVR 60
Db 1 MTEQAISFADFLAGIAAISTAVAPIERVKLLQVQHASKOIADKQYKGIIVDCIVR 60
Qy 61 IPKQGVLSFWRGNLANVIRFPPTQALNPAFKDKTKOIFLGVDKHTQFMRYFAGNLASG 120
Db 61 IPKQGVLSFWRGNLANVIRFPPTQALNPAFKDKTKOIFLGVDKHTQFMRYFAGNLASG 120
Qy 121 GAAGATSLCFYPPDLPARTLAADVKGSGTEREFGDCLVKTSGIKGLYOGFSVS 180
Db 121 GAAGATSLCFYPPDLPARTLAADVKGSGTEREFGDCLVKTSGIKGLYOGFSVS 180
Qy 181 VGGIITRAAFYGVYDTAKGMLPDPKNTHTIVSWMIAGTVAVAGVSYPPDYARRMM 240
Db 181 VGGIITRAAFYGVYDTAKGMLPDPKNTHTIVSWMIAGTVAVAGVSYPPDYARRMM 240
Qy 241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFFKGAMSNVLRMGGAFLVLYDELKVI 238
Db 241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFFKGAMSNVLRMGGAFLVLYDELKVI 238

RESULT 3
US-09-185-904A-33

Sequence 33, Application US/09185904A
Patent No. US20020177185A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.

APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
FILE REFERENCE: 660088.420
CURRENT APPLICATION NUMBER: US/09/185.904A
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-185-904A-33

Query Match 100.0%; Score 1543; DB 10; Length 298;
Best Local Similarity 100.0%; Pred. No. 1e-156;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTEQAISFADFLAGIAAISTAVAPIERVKLLQVQHASKOIADKQYKGIIVDCIVR 60
Db 1 MTEQAISFADFLAGIAAISTAVAPIERVKLLQVQHASKOIADKQYKGIIVDCIVR 60
Qy 61 IPKQGVLSFWRGNLANVIRFPPTQALNPAFKDKTKOIFLGVDKHTQFMRYFAGNLASG 120
Db 61 IPKQGVLSFWRGNLANVIRFPPTQALNPAFKDKTKOIFLGVDKHTQFMRYFAGNLASG 120
Qy 121 GAAGATSLCFYPPDLPARTLAADVKGSGTEREFGDCLVKTSGIKGLYOGFSVS 180
Db 121 GAAGATSLCFYPPDLPARTLAADVKGSGTEREFGDCLVKTSGIKGLYOGFSVS 180
Qy 181 VGGIITRAAFYGVYDTAKGMLPDPKNTHTIVSWMIAGTVAVAGVSYPPDYARRMM 240
Db 181 VGGIITRAAFYGVYDTAKGMLPDPKNTHTIVSWMIAGTVAVAGVSYPPDYARRMM 240
Qy 241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFFKGAMSNVLRMGGAFLVLYDELKVI 238
Db 241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFFKGAMSNVLRMGGAFLVLYDELKVI 238

RESULT 4
US-09-811-094-32

Sequence 32, Application US/09811094
Patent No. US20010044144A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pel, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D4
CURRENT APPLICATION NUMBER: US/09/811.094
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-811-094-32

Query Match 94.2%; Score 1454; DB 9; Length 298;
Best Local Similarity 92.6%; Pred. No. 3.5e-147;

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 31
LENGTH: 297
TYPE: PRF
ORGANISM: Homo sapien
US-09-811-094-31

Query Match 89.8%; Score 1385.5; DB 9; Length 297;
Best Local Similarity 87.2%; Pred. No. 7.5e-140;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

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QY 1 MTEQAISPAKDFLAGGIAAISTAVAPIERVKLLQVQHASKOIAADKQYKGIYDCIVR 60
DB 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEQYKGIIDCVRR 60
QY 61 IPKEGGLSFWRGNLANVIRYPTQALNFAFDKTKQIFLGVDHKGQFWRYPAGNLASG 120
DB 61 IPKEGGLSFWRGNLANVIRYPTQALNFAFDKTKQIFLGVDHKGQFWRYPAGNLASG 120
QY 121 GAAGTSLCFYVPLDPARTRLAADVGKSGTEREPGLDCLVTKTSGDGLRGLYOGFSVS 180
DB 121 GAAGTSLCFYVPLDPARTRLAADVGR-AGREPHGLDCLIKIFKSDGLRGLYOGFSVS 179
QY 181 VGGIITRYAAYFGYVDTAKGMLPDPKNTHTIVSWMIAGTVAAGVSPPTVRRRRMM 240
DB 180 VGGIITRYAAYFGYVDTAKGMLPDPKNTHTIVSWMIAGTVAAGVSPPTVRRRRMM 239
QY 241 QSGRGADIMYTGIVDCWRKIFRDEGKAFPKGAMSNVLRGGAFLVLYDELKVI 298
DB 240 QSGRGADIMYTGIVDCWRKIAKDEGAKAFPKGAMSNVLRGGAFLVLYDELKVI 297
```

RESULT 8

US-09-810-644-31
Sequence 31, Application US/09810644
Patent No. US20020012992A1

GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Cleenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pel, Yashong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT'),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D3
CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 31
LENGTH: 297
TYPE: PRF
ORGANISM: Homo sapien
US-09-810-644-31

Query Match 89.8%; Score 1385.5; DB 9; Length 297;
Best Local Similarity 87.2%; Pred. No. 7.5e-140;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

```
QY 1 MTEQAISPAKDFLAGGIAAISTAVAPIERVKLLQVQHASKOIAADKQYKGIYDCIVR 60
DB 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEQYKGIIDCVRR 60
QY 61 IPKEGGLSFWRGNLANVIRYPTQALNFAFDKTKQIFLGVDHKGQFWRYPAGNLASG 120
DB 61 IPKEGGLSFWRGNLANVIRYPTQALNFAFDKTKQIFLGVDHKGQFWRYPAGNLASG 120
QY 121 GAAGTSLCFYVPLDPARTRLAADVGKSGTEREPGLDCLVTKTSGDGLRGLYOGFSVS 180
DB 121 GAAGTSLCFYVPLDPARTRLAADVGKSGTEREPGLDCLVTKTSGDGLRGLYOGFSVS 180
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DB 121 GAAGTSLCFYVPLDPARTRLAADVGR-AGREPHGLDCLIKIFKSDGLRGLYOGFSVS 179
QY 181 VGGIITRYAAYFGYVDTAKGMLPDPKNTHTIVSWMIAGTVAAGVSPPTVRRRRMM 240
DB 180 VGGIITRYAAYFGYVDTAKGMLPDPKNTHTIVSWMIAGTVAAGVSPPTVRRRRMM 239
QY 241 QSGRGADIMYTGIVDCWRKIFRDEGKAFPKGAMSNVLRGGAFLVLYDELKVI 298
DB 240 QSGRGADIMYTGIVDCWRKIAKDEGAKAFPKGAMSNVLRGGAFLVLYDELKVI 297
```

RESULT 9

US-09-185-904A-31
Sequence 31, Application US/09185904A
Patent No. US2002017185A1

GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Cleenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLOCATOR (ANT'), NOVEL ANT LIGANDS AND SCREENING ASSAYS
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 660088.420
CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 31
LENGTH: 297
TYPE: PRF
ORGANISM: Homo sapien
US-09-185-904A-31

Query Match 89.8%; Score 1385.5; DB 10; Length 297;
Best Local Similarity 87.2%; Pred. No. 7.5e-140;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

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QY 1 MTEQAISPAKDFLAGGIAAISTAVAPIERVKLLQVQHASKOIAADKQYKGIYDCIVR 60
DB 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVQHASKOISAEQYKGIIDCVRR 60
QY 61 IPKEGGLSFWRGNLANVIRYPTQALNFAFDKTKQIFLGVDHKGQFWRYPAGNLASG 120
DB 61 IPKEGGLSFWRGNLANVIRYPTQALNFAFDKTKQIFLGVDHKGQFWRYPAGNLASG 120
QY 121 GAAGTSLCFYVPLDPARTRLAADVGKSGTEREPGLDCLVTKTSGDGLRGLYOGFSVS 180
DB 121 GAAGTSLCFYVPLDPARTRLAADVGR-AGREPHGLDCLIKIFKSDGLRGLYOGFSVS 179
QY 181 VGGIITRYAAYFGYVDTAKGMLPDPKNTHTIVSWMIAGTVAAGVSPPTVRRRRMM 240
DB 180 VGGIITRYAAYFGYVDTAKGMLPDPKNTHTIVSWMIAGTVAAGVSPPTVRRRRMM 239
QY 241 QSGRGADIMYTGIVDCWRKIFRDEGKAFPKGAMSNVLRGGAFLVLYDELKVI 298
DB 240 QSGRGADIMYTGIVDCWRKIAKDEGAKAFPKGAMSNVLRGGAFLVLYDELKVI 297
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RESULT 10

US-10-029-386-32501
Sequence 32501, Application US/10029386
Publication No. US2003019470A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: ABOIMCA-X-2

```
;; CURRENT APPLICATION NUMBER: US/10/029,386
;; CURRENT FILING DATE: 2001-12-20
;; NUMBER OF SEQ ID NOS: 34288
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 32501
;; LENGTH: 179
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC004000.1
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
;; OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 3.5
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.95
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96
;; OTHER INFORMATION: SWISSPROT HIT: P05141, EVALU2 2.00e-83
US-10-029-386-32501

Query Match          52.6%; Score 811; DB 12; Length 179;
Best Local Similarity 93.3%; Pred. No. 1.2e-78;
Matches 152; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

OY 38 VQASKOIADKQYKGIYDQIVRIPKQGVLSFMRGNLANYRYPPQALNPAFKQKXKQ 97
DB 1 VQASKOIADKQYKGIYDQIVRIPKQGVLSFMRGNLANYRYPPQALNPAFKQKXKQ 60
OY 98 IFLGVDHGTQPMRYFAENLASGGAAGTSLCFYVPLDPARTRLAADVGKSTREPRGL 157
DB 61 IFLGVDHGTQPMRYFAENLASGGAAGTSLCFYVPLDPARTRLAADVGKSTREPRGL 120
OY 158 GDCLVTKIKSDGIRGLYQGSFVSVOGIIIRAAVFGVYDTAKG 200
DB 121 GDCLVTKIKSDGIRGLYQGSFVSVOGIIIRAAVFGVYDTAKG 163

RESULT 11
US-10-032-585-7194
;; Sequence 7194, Application US/10032585
;; Publication No. US20030180953A1
;; GENERAL INFORMATION:
;; APPLICANT: Terry, Roemer D.
;; APPLICANT: Bo, Jlang
;; APPLICANT: Charles, Boone
;; APPLICANT: Howard, Bussey
;; TITLE OR INVENTION: Gene Disruption Methodologies for Drug Target Discovery
;; FILE REFERENCE: 10182-005-999
;; CURRENT APPLICATION NUMBER: US/10/032,585
;; CURRENT FILING DATE: 2001-12-20
;; NUMBER OF SEQ ID NOS: 8000
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 7194
;; LENGTH: 301
;; TYPE: PRT
;; ORGANISM: Candida albicans
US-10-032-585-7194

Query Match          51.1%; Score 788.5; DB 12; Length 301;
Best Local Similarity 54.7%; Pred. No. 6.3e-76;
Matches 162; Conservative 42; Mismatches 83; Indels 9; Gaps 5;

OY 7 SFADPLAGGIAAISTKTAVALPIERVKLLQVQ--HASKQIADKQYKGIYDQIVRIPKQ 65
DB 5 NFADPLAGGIAAISTKTAVALPIERVKLLQVQ--HASKQIADKQYKGIYDQIVRIPKQ 64
OY 66 GVLSPFRGNLANVIRYPPQALNPAFKQYKQIFLGVDHGTQPMRYFAENLASGGAAGA 125
DB 65 GVLSPFRGNLANVIRYPPQALNPAFKQYKQIFLGVDHGTQPMRYFAENLASGGAAGA 122
OY 126 TSLCFYVPLDPARTRLAADV--GKSGTEREPRGLDCLVTKISDGRIGLYQGSFVSVOG 183
DB 123 TSLCFYVPLDPARTRLAADV--GKSGTEREPRGLDCLVTKISDGRIGLYQGSFVSVOG 182
OY 184 IIRAAVFGVYDTAKG--MLPDPKNTTHIVSWMIAQVTAAGVAVSYPPFVRRRRMMQ 242
```

```
DB 183 IIVYRGILYFGLYDGLKVLVLCPIEGSFLASFLILGAVTTGASTASVPLDVRRRMMQ 242
OY 243 GRKADIMYTGTVDCWKIRFBDGSKAFPFKGANSNVRIGKGAFAVLVYDELKVTI 298
DB 243 GQA---VKYDGAIDCFRKYVAABGVSLPFKGCAGNIIRGVAGAVISLYDQLQVTL 295

RESULT 12
US-09-801-368-252
;; Sequence 252, Application US/09801368
;; Patent No. US20020128250A1
;; GENERAL INFORMATION:
;; APPLICANT: Bueby, Robert
;; APPLICANT: Cali, Brian
;; APPLICANT: Hecht, Peter
;; APPLICANT: Holtzman, Doug
;; APPLICANT: Madden, Kevin
;; APPLICANT: Maxon, Mary
;; APPLICANT: Milne, Todd
;; APPLICANT: No. US20020128250A1man, Thea
;; APPLICANT: Royer, John
;; APPLICANT: Salama, Sofie
;; APPLICANT: Sherman, Amir
;; APPLICANT: Silva, Jeff
;; APPLICANT: Summers, Eric
;; TITLE OR INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
;; FILE REFERENCE: 109272.147
;; CURRENT APPLICATION NUMBER: US/09/801,368
;; CURRENT FILING DATE: 2001-03-07
;; PRIOR APPLICATION NUMBER: US 09/487,558
;; PRIOR FILING DATE: 2000-01-19
;; PRIOR APPLICATION NUMBER: US 60/160,587
;; NUMBER OF SEQ ID NOS: 440
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 252
;; LENGTH: 318
;; TYPE: PRT
;; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-252

Query Match          49.3%; Score 760.5; DB 10; Length 318;
Best Local Similarity 53.7%; Pred. No. 6.8e-73;
Matches 159; Conservative 42; Mismatches 86; Indels 9; Gaps 5;

OY 7 SFADPLAGGIAAISTKTAVALPIERVKLLQVQ--HASKQIADKQYKGIYDQIVRIPKQ 65
DB 22 NFADPLAGGIAAISTKTAVALPIERVKLLQVQ--HASKQIADKQYKGIYDQIVRIPKQ 81
OY 66 GVLSPFRGNLANVIRYPPQALNPAFKQYKQIFLGVDHGTQPMRYFAENLASGGAAGA 125
DB 82 GVLSPFRGNLANVIRYPPQALNPAFKQYKQIFLGVDHGTQPMRYFAENLASGGAAGA 139
OY 126 TSLCFYVPLDPARTRLAADV--GKSGTEREPRGLDCLVTKISDGRIGLYQGSFVSVOG 183
DB 140 TSLCFYVPLDPARTRLAADV--GKSGTEREPRGLDCLVTKISDGRIGLYQGSFVSVOG 199
OY 184 IIRAAVFGVYDTAKG--MLPDPKNTTHIVSWMIAQVTAAGVAVSYPPFVRRRRMMQ 242
DB 200 IIVYRGILYFGLYDGLKVLVLCPIEGSFLASFLILGAVTTGASTASVPLDVRRRMMQ 259
OY 243 GRKADIMYTGTVDCWKIRFBDGSKAFPFKGANSNVRIGKGAFAVLVYDELKVTI 298
DB 260 GQA---VKYDGAIDCFRKYVAABGVSLPFKGCAGNIIRGVAGAVISLYDQLQVTL 312

RESULT 13
US-09-734-569-170
;; Sequence 170, Application US/09734569
;; Patent No. US20020064816A1
;; GENERAL INFORMATION:
;; APPLICANT: Lerchl, Jens
```

APPLICANT: Reut, Andreas
APPLICANT: Ehrhardt, Thomas
APPLICANT: Reindl, Andreas
APPLICANT: Cirus, Petra
APPLICANT: Bischoff, Friedrich
APPLICANT: Frank, Markus
APPLICANT: Freund, Annette
APPLICANT: Duwenig, Elke
APPLICANT: Schmidt, Ralf-Michael
APPLICANT: Reeski, Ralf
TITLE OF INVENTION: Moss genes from *Physcomitrella patens* encoding proteins involved
in the synthesis of carbohydrates
FILE REFERENCE: BASF-NR-1333-99-US
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US/09/734,569
PRIOR FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 181
SOFTWARE: PatentIn Ver. 2.1/WordPerfect 6.1
SEQ ID NO 170
LENGTH: 386
TYPE: PRT
ORGANISM: *Physcomitrella patens*
US-09-734-569-170

Query Match 48.6%; Score 749.5; DB 9; Length 386;
Best Local Similarity 53.4%; Pred. No. 1.3e-71;
Matches 157; Conservative 44; Mismatches 84; Indels 9; Gaps 5;

Cy 7 SPADFLAGIAGIAAISTKAVAPIERVKLLQVQ-HASQIADAKQYKIVDCIARIPEKQ 65
Db 84 SPMDFLWGVSAVSKTAAPIERVKLLIQVQDEMLKSGRLSHPEYKIGECFSTVYKQ 143
Cy 66 GVLSFWRGNLAVIRYPTQALNFAFKQYKQIFLGVDKHTQFWRYPAGNLASGAAGA 125
Db 144 GMSLWGRNTAVIRYPTQALNFAFKQYKQIFLGVDKHTQFWRYPAGNLASGAAGA 202
Cy 126 TSLCFTYPLDPAKRTLAADV--GKSGTEREPRGIDCLVKTYSKDGIRGLYQGSVSQ 182
Db 203 SSLFVYSLDPAKRTLAADV--GKSGTEREPRGIDCLVKTYSKDGIRGLYQGSVSQ 262
Cy 183 GIITRYAAYFGVYDPAK--MLPDPKNTIIVSWMIAQTVAAGVSYPTVRRMMQ 241
Db 263 GIITRYGAYFGVYDPAK--MLPDPKNTIIVSWMIAQTVAAGVSYPTVRRMMQ 322
Cy 242 SGRKADIMYTGVDCKRKIFRDEGKAFPKGAMSVLRMGAFVLVYDELK 295
Db 323 SGRA--VKYNGSMDAFKQILAKGAKSLFKGAGANILRAVAGAVLSGYDQLQ 373

RESULT 14
US-10-128-714-3338
Sequence 3338, Application US/10128714
Publication No. US20030119013A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Hu, Wengqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in *Aspergillus fumigatus* and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US/10/128,714
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899

PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3338
LENGTH: 308
TYPE: PRT
ORGANISM: *Aspergillus fumigatus*
US-10-128-714-3338

Query Match 47.8%; Score 737; DB 15; Length 308;
Best Local Similarity 51.7%; Pred. No. 2.1e-70;
Matches 154; Conservative 47; Mismatches 85; Indels 12; Gaps 6;

Cy 7 SPADFLAGIAGIAAISTKAVAPIERVKLLQVQHASQIADAKQYKIVDCIARIPEK 63
Db 7 APTDSPAAGVSAVSKTAAPIERVKLL--VQNDQEMIRAGRLDRKNGIIDCFRRRAQ 64
Cy 64 ECVLSFWRGNLAVIRYPTQALNFAFKQYKQIFLGVDKHTQFWRYPAGNLASGAAGA 123
Db 65 AEGVMSLWGRNTAVIRYPTQALNFAFKQYKQIFLGVDKHTQFWRYPAGNLASGAAGA 123
Cy 124 GATSLCFTYPLDPAKRTLAADV--GKSGTEREPRGIDCLVKTYSKDGIRGLYQGSVSQ 181
Db 124 GATSLCFTYPLDPAKRTLAADV--GKSGTEREPRGIDCLVKTYSKDGIRGLYQGSVSQ 183
Cy 182 GIIITRYAAYFGVYDPAK--MLPDPKNTIIVSWMIAQTVAAGVSYPTVRRMMQ 240
Db 184 LGITVYSLDPAKRTLAADV--GKSGTEREPRGIDCLVKTYSKDGIRGLYQGSVSQ 243
Cy 241 QSGRKADIMYTGVDCKRKIFRDEGKAFPKGAMSVLRMGAFVLVYDELK 298
Db 244 TSGBA--VKYKSLDAKQILAKGAKSLFKGAGANILRAVAGAVLSGYDQLQ 298

RESULT 15
US-10-128-714-8338
Sequence 8338, Application US/10128714
Publication No. US20030119013A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Hu, Wengqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in *Aspergillus fumigatus* and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US/10/128,714
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8338
LENGTH: 308
TYPE: PRT
ORGANISM: *Aspergillus fumigatus*
US-10-128-714-8338

Query Match 47.8%; Score 737; DB 15; Length 308;
Best Local Similarity 51.7%; Pred. No. 2.1e-70;
Matches 154; Conservative 47; Mismatches 85; Indels 12; Gaps 6;

```

Oy 7 SPAKDFLAGIAAISTAVAPIERVKLLLOYHASKOIAA--DKOYKGIYDCIWRIPK 63
Db 7 APTDSFVAVGVSAASKTAAAFIERIKLL--VONODEMIRAGRLDRKTNGLIDCFRRTAQ 64
Oy 64 BOGVLSPWRGNLANVIRYFPTOLNFAFKDKYKQIFLGVDKHTQFMWRYFAGNLASGGAA 123
Db 65 AEGVMSLWRGNLANVIRYFPTOLNFAFRDLYKSMFAYKOR-DGYAKMMGNLASGGAA 123
Oy 124 GATSLCFYYPIDFARTLAADV--GKSGTEREFRLGDLVKITKSDGIRGLYOGFSVSV 181
Db 124 GATSLLPYSLDYARTLANDAKSAGGGERQFNGLIDVYRKTLASDGIAGLYRGFGPSV 183
Oy 182 OGIIYRAAYFGVYDTAKG-MLPDPKXTHIVSWMLAQVTYAVAGVSYPPEDTVRRMM 240
Db 184 LGIVYTRGLYFGMTDSIKFVVLVGSLEGSFLASFLGWTVTTGAGIASYPLDTIRRRMM 243
Oy 241 QSGRKGADIMYTGVCWRKIFRDEGGAFAFKGAMSNVLRGNGAFVLVLYDELKVI 298
Db 244 TSGBA--VKYKSSLDAAKQIIAKEGVKSLFKGAGANTLRGVAAGVLSIYDQVQLL 298

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Search completed: December 18, 2003, 12:55:44
 Job time : 25.3606 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:37:46 ; Search time 14.3494 Seconds
(without alignments)
1997.178 Million cell updates/sec

Title: US-09-811-131-33

Perfect score: 1543
Sequence: 1 MTEGAISFADPLAGTAA.....LRGNGAFVLYVDELKVI 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR 76:*

1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	100.0	298	1	S03894 ADP,ATP carrier pr
2	1512	98.0	298	1	B43646 ADP,ATP carrier pr
3	1454	94.2	298	1	A29132 ADP,ATP carrier pr
4	1424	92.3	298	2	I60173 adenine nucleotide
5	1422	92.2	298	1	XWBO ADP,ATP carrier pr
6	1418	91.9	298	2	S37210 ADP,ATP carrier pr
7	1409	91.3	298	1	A44778 ADP,ATP carrier pr
8	1405	91.1	298	2	S31814 ADP,ATP carrier pr
9	1184	76.7	301	1	S31935 ADP,ATP carrier pr
10	1041	67.5	313	2	T23207 ADP,ATP carrier pr
11	1039	67.3	313	2	T25850 hypothetical prote
12	1038	67.3	300	2	T25371 hypothetical prote
13	993.5	64.4	300	2	T15206 hypothetical prote
14	943	63.4	339	2	A41677 ADP,ATP carrier pr
15	943	61.1	301	2	S51132 ADP,ATP carrier pr
16	778.5	50.5	307	2	A36582 ADP,ATP carrier pr
17	772	50.0	308	1	S30259 ADP,ATP carrier pr
18	769	49.8	322	2	T40526 adp/atp translocas
19	768	49.8	386	2	ADP,ATP carrier pr
20	766	49.6	313	1	XWNC ADP,ATP carrier pr
21	764	49.4	326	2	T25728 hypothetical prote
22	762.5	49.4	305	2	S68154 ADP,ATP carrier pr
23	760.5	49.3	318	1	A31978 ADP,ATP carrier pr
24	756.5	49.0	306	2	T20012 hypothetical prote
25	750	48.6	387	2	S14876 ADP,ATP carrier pr
26	748	48.5	386	2	S21974 ADP,ATP carrier pr
27	747	48.4	306	2	T42011 ADP,ATP carrier pr
28	747	48.4	386	2	S17917 ADP,ATP carrier pr
29	744	48.2	387	2	S16568 ADP,ATP carrier pr

30	743	48.2	379	2	T04608 ADP,ATP carrier pr
31	742.5	48.1	385	1	S29852 ADP,ATP carrier pr
32	742	48.1	382	2	S33630 ADP,ATP carrier pr
33	739.5	47.9	386	2	S14874 ADP,ATP carrier pr
34	737.5	47.8	309	2	A24849 ADP,ATP carrier pr
35	734.5	47.6	379	2	S21313 ADP,ATP carrier pr
36	681.5	44.2	298	2	T24029 hypothetical prote
37	520.5	33.7	327	2	T51577 ADP/ATP translocas
38	383	24.8	325	2	T04273 hypothetical prote
39	381	24.7	352	2	T01729 mitochondrial solu
40	372	24.1	358	2	T45934 hypothetical prote
41	370.5	24.0	415	2	T48171 hypothetical prote
42	369.5	23.9	381	2	T51158 hypothetical prote
43	368	23.8	475	2	T50686 peroxisomal Ca-dep
44	363	23.5	348	2	D84798 probable mitochond
45	344.5	22.3	332	2	T47703 Ca-dependent solut

ALIGNMENTS

RESULT 1

S03894
ADP,ATP carrier protein T3 - human
N/Alternate names: ADP,ATP carrier protein T2 (misidentification); mitochondrial ADP,ATP
C/Species: Homo sapiens (man)
C/Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C/Accession: S03894; B28116
R/Cozens, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A/Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr
A/Reference number: S03893; MUID:69236396; PMID:2541251
A/Accession: S03894
A/Status: not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-298 <CO2>
R/Houldsworth, J.; Attard, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A/Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a
A/Reference number: A94197; MUID:88124845; PMID:2829183
A/Accession: B28116
A/Molecule type: mRNA
A/Residues: 36-104, 'R', 106, 'A', 109-298 <HOU>
A/Cross-references: GB:J03552; NID:g339722; PIDN:AAA36750.1; PID:g339723
A/Experimental source: liver
C/Genetics:
A/Gene: GDB:ANT3; ANT3Y
A/Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
A/Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and GDB:
C/Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C/Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F/2-298/Product: ADP,ATP carrier protein #stratus predicted <MAT>
F/5-99/Domains: ADP,ATP carrier protein repeat homology <ACP1>
F/110-202/Domains: ADP,ATP carrier protein repeat homology <ACP2>
F/207-298/Domains: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 100.0%; Score 1543; DB 1; Length 298;

Best Local Similarity 100.0%; Pred. No. 6e-129;

Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MTEGAISFADPLAGTAAISTAVPIERVKLLLOVQHASKOIADKQYGIIVDCIVR	60
Db	1	MTEGAISFADPLAGTAAISTAVPIERVKLLLOVQHASKOIADKQYGIIVDCIVR	60
Qy	61	IPKQGVLSFMRGNLAVIYFPPTQALNPAFKQCYKQIFPGVYDKHQPFRYFAGNLASG	120
Db	61	IPKQGVLSFMRGNLAVIYFPPTQALNPAFKQCYKQIFPGVYDKHQPFRYFAGNLASG	120
Qy	121	GAAGATSLCFVYPLDFARTLADVQKSGTEREERFGIDCLVKTGSDGIRGLYQGSVS	180
Db	121	GAAGATSLCFVYPLDFARTLADVQKSGTEREERFGIDCLVKTGSDGIRGLYQGSVS	180

QY 61 IPKGGVLSFMRGNLANVIRYPTQALNFAKDKYKQIFLGVDKHTQFWRFAGNLSG 120
DB 61 IPKGGVLSFMRGNLANVIRYPTQALNFAKDKYKQIFLGVDKHTQFWRFAGNLSG 120
QY 121 GAAGATSLCFVYPLDPFATRLAADVGKSGTEREFRGLDCLVKITKSDGIRGLYOGFSVS 180
DB 121 GAAGATSLCFVYPLDPFATRLAADVGKSGSGREFRGLDCLVKITKSDGIRGLYOGFSVS 180
QY 181 VGGIITRYAAAFYGVYDTRAKGMLPDPKNTHTIVSMIAQCTVAAGVSYPPDTRRRMM 240
DB 181 VGGIITRYAAAFYGVYDTRAKGMLPDPKNTHTIVSMIAQCTVAAGVSYPPDTRRRMM 240
QY 241 OSGRKADIMVTGTVDGCRKIFRDEGKAFKFGKAMSNVLRGKGAFLVLYDELKKVI 298
DB 241 OSGRKADIMVTGTVDGCRKIFRDEGKAFKFGKAMSNVLRGKGAFLVLYDELKKVI 298

RESULT 5

KWBO
ADP, ATP carrier protein T1 - bovine
N/Alternate names: ADP/ATP translocase T1
C/Species: Bos primigenius taurus (cattle)
C/Date: 14-Nov-1983 #sequence revision 22-Jul-1994 #text_change 22-Jun-1999
R/Accession: A43646; A24822; A03181; A61343; S69369
R/Powell, S.J.; Mead, S.M.; Runswick, M.J.; Walker, J.B.
Biochemistry 26, 866-873, 1989
A/Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
A/Reference number: A43646; MUID:89229093; PMID:2540808
A/Accession: A43646
A/Molecule type: mRNA
A/Residues: 1-298 <POW>
A/Cross-references: GB:M24102; NID:9529414; PIDN:AAA30768.1; PID:9529415
R/Rasmussen, U.B.; Wolfrum, H.
Biochem. Biophys. Res. Commun. 138, 850-857, 1986
A/Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unusual
A/Reference number: A24822; MUID:86295775; PMID:3017341
A/Accession: A24822
A/Molecule type: mRNA
A/Residues: 208-298 <RAS>
A/Cross-references: GB:M13783; NID:9162630; PIDN:AAA0363.1; PID:9162631
R/Aquila, H.; Maser, D.; Bulitz, M.; Klingenberg, M.
Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982
A/Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondria
A/Reference number: A03181; MUID:82188267; PMID:7076130
A/Accession: A03181
A/Molecule type: Protein
A/Residues: 2-51, 'X', '53-70', 'X', '72-109', 'X', '111-298 <AGU>
A/Note: residue 52 may be methyllysine
R/Babel, W.; Wachter, B.; Aquila, H.; Klingenberg, M.
Biochim. Biophys. Acta 670, 176-180, 1981
A/Title: Amino acid sequence determination of the ADP/ATP carrier from beef heart mitochondria
A/Reference number: A61343; MUID:82046808; PMID:6271240
A/Accession: A61343
A/Molecule type: Protein
A/Residues: 205-298 <BAB>
R/Oettermeyer, W.; Nasson, K.; Kalima, S.
Eur. J. Biochem. 227, 730-733, 1995
A/Title: (3)H/7-azido-4-isopropylacridone labels Cys159 of the bovine mitochondrial ADP
A/Reference number: S69369; MUID:95172058; PMID:7867632
A/Accession: S69369
A/Molecule type: protein
A/Residues: 49-63;154-168 <OET>
C/Comment: This protein is synthesized in the cytosol and transported into the mitochondrion
C/Complex: homodimer
C/Function:
A/Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP genera
C/Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
C/Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mitoch
F/110-202/Domain: ADP, ATP carrier protein repeat homology <ACP1>
F/110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>
F/207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

F/2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
F/52/Modified site: N6-methyllysine (lys) #status predicted

Query Match 92.2%; Score 1422; DB 1; Length 298;
Best Local Similarity 89.3%; Pred. No. 3.1e-118;
Matches 266; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEQALSPAKDPLAGGIAAISKTAIVPIREVKLLIQVHASKQIADKQKGIYDCTVR 60
DB 1 MSDQALSPKDFLAGGVAIAISKTAIVPIREVKLLIQVHASKQISAEKQYKGIIDCVVR 60
QY 61 IPKGGVLSFMRGNLANVIRYPTQALNFAKDKYKQIFLGVDKHTQFWRFAGNLSG 120
DB 61 IPKGGVLSFMRGNLANVIRYPTQALNFAKDKYKQIFLGVDKHTQFWRFAGNLSG 120
QY 121 GAAGATSLCFVYPLDPFATRLAADVGKSGTEREFRGLDCLVKITKSDGIRGLYOGFSVS 180
DB 121 GAAGATSLCFVYPLDPFATRLAADVGKSGSGREFRGLDCLVKITKSDGIRGLYOGFSVS 180
QY 181 VGGIITRYAAAFYGVYDTRAKGMLPDPKNTHTIVSMIAQCTVAAGVSYPPDTRRRMM 240
DB 181 VGGIITRYAAAFYGVYDTRAKGMLPDPKNTHTIVSMIAQCTVAAGVSYPPDTRRRMM 240
QY 241 OSGRKADIMVTGTVDGCRKIFRDEGKAFKFGKAMSNVLRGKGAFLVLYDELKKVI 298
DB 241 OSGRKADIMVTGTVDGCRKIFRDEGKAFKFGKAMSNVLRGKGAFLVLYDELKKVI 298

RESULT 6

S37210
ADP, ATP carrier protein T1 - mouse
N/Alternate names: adenine nucleotide carrier
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 20-Aug-1999
R/Laplace, C.; Costet, P.
submitted to the EMBL Data Library, September 1993
A/Reference number: S37210
A/Accession: S37210
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-298 <LAP>
A/Cross-references: EMBL:X74510; NID:9402627; PIDN:CAA52616.1; PID:9402628
C/Genetic: ANCI
A/Gene: ANCI
C/Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
C/Keywords: duplication; transmembrane protein
F/5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>
F/110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>
F/207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>
Query Match 91.9%; Score 1418; DB 2; Length 298;
Best Local Similarity 88.9%; Pred. No. 6.9e-118;
Matches 265; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTEQALSPAKDPLAGGIAAISKTAIVPIREVKLLIQVHASKQIADKQKGIYDCTVR 60
DB 1 MGDQALSPKDFLAGGVAIAISKTAIVPIREVKLLIQVHASKQISAEKQYKGIIDCVVR 60
QY 61 IPKGGVLSFMRGNLANVIRYPTQALNFAKDKYKQIFLGVDKHTQFWRFAGNLSG 120
DB 61 IPKGGVLSFMRGNLANVIRYPTQALNFAKDKYKQIFLGVDKHTQFWRFAGNLSG 120
QY 121 GAAGATSLCFVYPLDPFATRLAADVGKSGTEREFRGLDCLVKITKSDGIRGLYOGFSVS 180
DB 121 GAAGATSLCFVYPLDPFATRLAADVGKSGSGREFRGLDCLVKITKSDGIRGLYOGFSVS 180
QY 181 VGGIITRYAAAFYGVYDTRAKGMLPDPKNTHTIVSMIAQCTVAAGVSYPPDTRRRMM 240
DB 181 VGGIITRYAAAFYGVYDTRAKGMLPDPKNTHTIVSMIAQCTVAAGVSYPPDTRRRMM 240
QY 241 OSGRKADIMVTGTVDGCRKIFRDEGKAFKFGKAMSNVLRGKGAFLVLYDELKKVI 298
DB 241 OSGRKADIMVTGTVDGCRKIFRDEGKAFKFGKAMSNVLRGKGAFLVLYDELKKVI 298

Db 241 OSGRKADIMTGTGTCCKRIKADBGANAFKFGAMSNVLRMGCAFVLVYDEIKCY 298

RESULT 7

ADP/ATP carrier protein T1 - human
N/Alternate names: mitochondrial ADP/ATP translocase 1
C/Species: Homo sapiens (man)
C/Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C/Accession: A44778; S03893; A39891; A28116
R/L1: K.; Warner, C.K.; Hodges, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, M.
J. Biol. Chem. 264, 13998-14004, 1999
A/Title: A human muscle adenine nucleotide translocator gene has four exons, is located
A/Reference number: A44778; MUID:89340499; PMID:2547778
A/Accession: A44778
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-298 <L1>
A/Cross-references: GB:J04982; NID:9178658; PIDN:AAA51736.1; PID:9178659
R/Cozen, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A/Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr
A/Reference number: S03893; MUID:8936396; PMID:2541251
A/Accession: S03893
A/Status: not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-298 <CO2>
R/Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.
Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987
A/Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader
A/Reference number: A39891; MUID:88041149; PMID:2832266
A/Accession: A39891
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-25, 'A', 17-146, 'RR', 149, 151-226, 'L', 228-298 <NEC>
A/Cross-references: GB:J02986; NID:933919; PIDN:AAA61223.1; PID:933920
R/Experimental source: clone PHMANT
R/Houldsworth, J.; Altardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A/Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a
A/Reference number: A4197; MUID:88124845; PMID:2829183
A/Accession: A28116
A/Molecule type: mRNA
A/Residues: 1-37 <HOU>
A/Cross-references: GB:J03593; NID:9339724; PIDN:AAA6751.1; PID:9339725
A/Experimental source: liver
C/Genetics:
A/Genes: GDB:ANT1, T1
A/Cross-references: GDB:119680; OMIM:103220
A/Map position: 4q35-4q35
C/Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
C/Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F/2-298/Domain: ADP/ATP carrier protein status predicted <MNT>
F/5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>
F/110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
F/207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 91.3%; Score 1409; DB 1; Length 298;
Best Local Similarity 88.3%; Pred. No. 4, 3e-117;
Matches 263; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MTEQASFAKDFLAGGIAAISKTAAPRERKLLQVQHASKQIAADKQYKGIYDCYR 60
Db 1 MGDHMSFLKDFLAGGVAASKTAAPRERKLLQVQHASKQIAADKQYKGIYDCYR 60
Qy 61 IPKEGVLSFPRGNLANVIRYPTQALNFAFDKTKQIFLGVDVGHQTFMRYPAGNLASG 120
Db 61 IPKEGVLSFPRGNLANVIRYPTQALNFAFDKTKQIFLGVDVGHQTFMRYPAGNLASG 120
Qy 121 GAAGATSCFYYPIDFATRIAADVKGSGTERPRGIDCVTKIKSDGIRGLYOGFSFVS 180
Db 121 GAAGATSCFYYPIDFATRIAADVKGSGTERPRGIDCVTKIKSDGIRGLYOGFSFVS 180

Qy 181 VGGIIYAAAFGYVDTKAGMLPDPKXTHIVVSMIAQTYTAAVAGVSPYPTVRRMM 240
Db 181 VGGIIYAAAFGYVDTKAGMLPDPKXTHIVVSMIAQTYTAAVAGVSPYPTVRRMM 240
Qy 241 OSGRKADIMTGTGTCCKRIKADBGANAFKFGAMSNVLRMGCAFVLVYDEIKCY 298
Db 241 OSGRKADIMTGTGTCCKRIKADBGANAFKFGAMSNVLRMGCAFVLVYDEIKCY 298

RESULT 8

ADP/ATP carrier protein T2 - mouse
N/Alternate names: adenine nucleotide translocase
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Apr-1998
C/Accession: S31814
R/Coates, P.; Laplace, C.
submitted to the EMBL Data Library, January 1993
A/Reference number: S31814
A/Accession: S31814
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-298 <COS>
A/Cross-references: EMBL:X70847
C/Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
C/Keywords: duplication; transmembrane protein
F/5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>
F/110-202/Domain: ADP/ATP carrier protein repeat homology <ACP>
F/207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 91.1%; Score 1405; DB 2; Length 298;
Best Local Similarity 89.2%; Pred. No. 9, 8e-117;
Matches 264; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MTEQASFAKDFLAGGIAAISKTAAPRERKLLQVQHASKQIAADKQYKGIYDCYR 60
Db 1 MTDNAVFAKDFLAGGVAASKTAAPRERKLLQVQHASKQIAADKQYKGIYDCYR 60
Qy 61 IPKEGVLSFPRGNLANVIRYPTQALNFAFDKTKQIFLGVDVGHQTFMRYPAGNLASG 120
Db 61 IPKEGVLSFPRGNLANVIRYPTQALNFAFDKTKQIFLGVDVGHQTFMRYPAGNLASG 120
Qy 121 GAAGATSCFYYPIDFATRIAADVKGSGTERPRGIDCVTKIKSDGIRGLYOGFSFVS 180
Db 121 GAAGATSCFYYPIDFATRIAADVKGSGTERPRGIDCVTKIKSDGIRGLYOGFSFVS 180
Qy 181 VGGIIYAAAFGYVDTKAGMLPDPKXTHIVVSMIAQTYTAAVAGVSPYPTVRRMM 240
Db 181 VGGIIYAAAFGYVDTKAGMLPDPKXTHIVVSMIAQTYTAAVAGVSPYPTVRRMM 240
Qy 241 OSGRKADIMTGTGTCCKRIKADBGANAFKFGAMSNVLRMGCAFVLVYDEIKCY 296
Db 241 OSGRKADIMTGTGTCCKRIKADBGANAFKFGAMSNVLRMGCAFVLVYDEIKCY 296

RESULT 9

ADP/ATP carrier protein - African malaria mosquito
C/Species: Anopheles gambiae (African malaria mosquito)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: S31935; S31936
R/Beard, C.B.; Crews-Oyen, A.E.; Collins, F.H.
submitted to the EMBL Data Library, February 1993
A/Description: A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae.
A/Reference number: S31935
A/Accession: S31935
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-301 <BEA>
A/Cross-references: EMBL:Z21814; EMBL:Z21815
C/Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
C/Keywords: duplication; transmembrane protein
F/7-101/Domain: ADP/ATP carrier protein repeat homology <ACP1>

F:112-204/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:209-300/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 76.7%; Score 1184; DB 1; Length 301;
Best Local Similarity 77.0%; Pred. No. 3.6e-97;
Matches 231; Conservative 23; Mismatches 44; Indels 2; Gaps 1;

QY 1 MTEQA--ISPAKDFLAGIAAISTKAVAPIERVKLLQVQHASKOIADKOYKGIYDCI 58
DB 1 MTKKADPRGFAKDFLAGISAAVSKTAVAPIERVKLLQVQHASKOIADKOYKGIYDCI 60
QY 59 VRIPEQVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKTKQFMRYPAGNTA 118
DB 61 VRIPEQIGAFCCGNLANVIRYPTQALNFAFKDVYKQVFLGVDKTKQFMRYPAGNTA 120
QY 119 SGGAAGATSLCFYVPLDPAFTRILADVSGSTEREPRLGDCIVKITSDDIRIGYQGRS 178
DB 121 SGGAAGATSLCFYVPLDPAFTRILGADVPGAGEERFNLDCIKTKVKSDDIIGLYRQFN 180
QY 179 VSVGGIITRYRAAYGVVDYAKGMLPDPKNTIIVVSMIAQVTVAVAGVSYPPDTRRRM 238
DB 181 VSVGGIITRYRAAYGVVDYAKGMLPDPKNTIIVVSMIAQVTVAVAGVSYPPDTRRRM 240
QY 239 MMQSGRKADIMYTGVDCKRKIFRDEGSKAFPKGAMSNVLRGKGAFVLVLYDELKXVI 298
DB 241 MMQSGRKADIMYTGVDCKRKIFRDEGSKAFPKGAMSNVLRGKGAFVLVLYDELKXVI 300

RESULT 10

T23207
hypothetical protein K01H12.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C:Accession: T23207

R:McMurray, A.
submitted to the EMBL Data Library, December 1995

A:Reference number: Z19707

A:Accession: T23207

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-313 <W1>

A:Cross-references: EMBL:Z68218; PIDN:CAA92472.1; GSPDB:GN00022; CESP:K01H12.2

A:Experimental source: clone K01H12

C:Genetics:

A:Gene: CESP:K01H12.2

A:Map position: 4

A:Insertions: 4/1; 191/2

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 67.5%; Score 1041; DB 2; Length 313;
Best Local Similarity 70.9%; Pred. No. 1.7e-84;

Matches 207; Conservative 29; Mismatches 52; Indels 4; Gaps 3;

QY 8 FAKDFLAGIAAISTKAVAPIERVKLLQVQHASKOIADKOYKGIYDCIIRIPKEQGV 67
DB 25 FLIDLAGGTAAASKTAVAPIERVKLLQVQDASLTIAADKRYKIVDVLRVPEKQGY 84
QY 68 LSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKTKQFMRYPAGNTASGGAAGATS 127
DB 85 AALMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKTKQFMRYPAGNTASGGAAGATS 144
QY 128 LCFYVPLDPAFTRILADVSGSTEREPRLGDCIVKITSDDIRIGYQGRS 187
DB 145 LCFYVPLDPAFTRILADVSGSTEREPRLGDCIVKITSDDIRIGYQGRS 203
QY 188 RAAFGVYDTAKGML-PDPKNTIIVVSMIAQVTVAVAGVSYPPDTRRRMMQSGRK 246
DB 204 RAAFGVYDTAKGML-PDPKNTIIVVSMIAQVTVAVAGVSYPPDTRRRMMQSGRK 262
QY 247 ADIMYTGVDCKRKIFRDEGSKAFPKGAMSNVLRGKGAFVLVLYDELKXVI 298
DB 263 -DVLVYKNTLDCAVKIIKKEGMSAMFKGALSIVFRGTGALVLAIDYDIQKFI 313

RESULT 11

T25850
hypothetical protein T01B11.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000

C:Accession: T25850

R:Geisel, C./ Stellye, L.

submitted to the EMBL Data Library, December 1996

A:Description: The sequence of C. elegans cosmid T01B11.

A:Reference number: Z20099

A:Accession: T25850

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-313 <GB1>

A:Cross-references: EMBL:U80931; PIDN:AB38001.1; GSPDB:GN00022; CESP:T01B11.4

A:Experimental source: strain Bristol N2; clone T01B11

C:Genetics:

A:Gene: CESP:T01B11.4

A:Map position: 4

A:Insertions: 4/1; 191/2

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 67.3%; Score 1039; DB 2; Length 313;
Best Local Similarity 70.9%; Pred. No. 2.6e-84;

Matches 207; Conservative 29; Mismatches 52; Indels 4; Gaps 3;

QY 8 FAKDFLAGIAAISTKAVAPIERVKLLQVQHASKOIADKOYKGIYDCIIRIPKEQGV 67
DB 25 FLIDLAGGTAAASKTAVAPIERVKLLQVQDASLTIAADKRYKIVDVLRVPEKQGY 84
QY 68 LSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKTKQFMRYPAGNTASGGAAGATS 127
DB 85 AALMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKTKQFMRYPAGNTASGGAAGATS 144
QY 128 LCFYVPLDPAFTRILADVSGSTEREPRLGDCIVKITSDDIRIGYQGRS 187
DB 145 LCFYVPLDPAFTRILADVSGSTEREPRLGDCIVKITSDDIRIGYQGRS 203
QY 188 RAAFGVYDTAKGML-PDPKNTIIVVSMIAQVTVAVAGVSYPPDTRRRMMQSGRK 246
DB 204 RAAFGVYDTAKGML-PDPKNTIIVVSMIAQVTVAVAGVSYPPDTRRRMMQSGRK 262
QY 247 ADIMYTGVDCKRKIFRDEGSKAFPKGAMSNVLRGKGAFVLVLYDELKXVI 298
DB 263 -DVLVYKNTLDCAVKIIKKEGMSAMFKGALSIVFRGTGALVLAIDYDIQKFI 313

RESULT 12

T25371
hypothetical protein T27B9.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000

C:Accession: T25371

R:Lloyd, C.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z20024

A:Accession: T25371

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-300 <W1>

A:Cross-references: EMBL:Z62059; PIDN:CA804874.1; GSPDB:GN00021; CESP:T27B9.1

A:Experimental source: clone T27B9

C:Genetics:

A:Gene: CESP:T27B9.1

A:Map position: 3

A:Insertions: 20/1; 41/3; 115/2

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 67.3%; Score 1038; DB 2; Length 300;
Best Local Similarity 69.2%; Pred. No. 3e-84;
Matches 202; Conservative 37; Mismatches 49; Indels 4; Gaps 3;

QY 8 PAKDPLAGGIAAISTKTAAPIERVKLLQVGHASKQIADKQYGVDCVIRIKEGV 67
 DB 12 FLIDIASGTAASVKTAVPIERVKLLQVODAKALAVDRYKGIWDLVIRKEGV 71
 QY 68 LSPFRGNLANVIRYPTQALNFAFKQKQIFLGVDKHTQFMRFPAGNLASGGAAGTS 127
 DB 72 AALMRGNLANVIRYPTQALNFAFKQKQIFLGVDKHTQFMRFPAGNLASGGAAGTS 131
 QY 128 LCFVYPLDPAFTRILADVGKSGTEREERGLDCLVKTSDGIRGLYOGFSVVOGIIIT 187
 DB 132 LCFVYPLDPAFTRILADVGKSGTEREERGLDCLVKTSDGIRGLYOGFSVVOGIIIT 190
 QY 188 RAAVGVVDPAKGL-PPKNTHTIVSMIAQTVTAAGVSPPTVRRMMQSGRG 246
 DB 191 RAAVGVVDPAKGL-PPKNTHTIVSMIAQTVTAAGVSPPTVRRMMQSGRG 249
 QY 247 ADIMYTGVDCKRKIFRDEGKAFKFGKAMSVNLKMGGAFLVLYDELKVI 298
 DB 250 -DILYKNTIDCKKIIQNEGMSAMFKGALSNVFRGTGALVLAIDEIKFL 300

RESULT 13

T15206

hypoheretical protein W0203.6 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000

C/Accession: T15206

R/ile, T.; Weinstein, L.; Riklin, L.

submitted to the EMBL Data Library, May 1997

A/Description: The sequence of C. elegans cosmid W0203.

A/Reference number: Z18308

A/Accession: T15206

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Residues: 1-300 <LET>

A/Cross-references: EMBL:AF003141; NID:G2088732; PID:G2088738; PIDN:AA54179.1; GSPDB:GN

A/Experimental source: strain Bristol N2; clone W0203

A/Genetic: 8

A/Map position: 1

C/Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

F/1-103/Domain: ADP, ATP carrier protein repeat homology <ACR>

Query Match 64.4%; Score 993.5; DB 2; Length 300;

Best Local Similarity 64.8%; Pred. No. 2.6e-80;

Matches 195; Conservative 40; Mismatches 59; Indels 7; Gaps 4;

QY 2 TEQAISPAK---DPLAGGIAAISTKTAAPIERVKLLQVGHASKQIADKQYGVDCI 58
 DB 3 TKEGFYRKLFLVDLASGGTAALISTKTAAPIERVKLLQVSDVSTVADKKYKIMDL 62
 QY 59 VRIPEQGVLSFWRGNLANVIRYPTQALNFAFKQKQIFLGVDKHTQFMRFPAGNLA 118
 DB 63 ARVPEQGVLSFWRGNLANVIRYPTQALNFAFKQKQIFLGVDKHTQFMRFPAGNLA 122
 QY 119 SGGAAGATSLCFVYPLDPAFTRILADVGKSGTEREERGLDCLVKTSDGIRGLYOGFS 178
 DB 123 SGGAAGATSLCFVYPLDPAFTRILADVGKSGTEREERGLDCLVKTSDGIRGLYOGFS 181
 QY 179 VSVQGIITVYRAVPEVVDPAKGL-PPKNTHTIVSMIAQTVTAAGVSPPTVRR 237
 DB 182 VSVQGIITVYRAVPEVVDPAKGL-PPKNTHTIVSMIAQTVTAAGVSPPTVRR 241
 QY 238 MMQSGRGKADIMYTGVDCKRKIFRDEGKAFKFGKAMSVNLKMGGAFLVLYDELKVI 297
 DB 242 MMQSGRK--DILYKNTIDCKKIIQNEGMSAMFKGALSNVFRGTGALVLAIDEIKFL 299

QY 298 I 298
 DB 300 I 300

RESULT 14

AA1677
 ADP, ATP carrier protein - Chlorella keesleri
 C/Species: Chlorella keesleri
 C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999
 C/Accession: AA1677
 R/Hilgath, C.; Sauer, N.; Tanner, W.
 J. Biol. Chem. 266, 24044-24047, 1991
 A/Title: Glucose increases the expression of the ATP/ADP translocator and the glyceralde
 A/Reference number: AA1677; MUID:92084708; PMID:1748677
 A/Accession: AA1677
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-339 <HT>
 A/Cross-references: GB:M76659; NID:G516596; PIDN:AA33027.1; PID:G516597
 C/Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
 C/Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F/38-134/Domain: ADP, ATP carrier protein repeat homology <ACPI>
 F/144-235/Domain: ADP, ATP carrier protein repeat homology <ACR2>
 F/241-329/Domain: ADP, ATP carrier protein repeat homology <ACR3>

Query Match

63.4%; Score 978; DB 2; Length 339;

Best Local Similarity 66.9%; Pred. No. 7.1e-79;

Matches 198; Conservative 26; Mismatches 64; Indels 8; Gaps 5;

QY 6 ISPAKDFLAGGIAAISTKTAAPIERVKLLQVGHASKQIADK--QYKGIYDCVIRIPK 63
 DB 39 MAFVYDLAAGTAAISTKTAAPIERVKLLQVODSNMISQVPRYTGIVNCFVRVS 98
 QY 64 EOGVLSFWRGNLANVIRYPTQALNFAFKQKQIFLGVDKHTQFMRFPAGNLASGGA 123
 DB 99 EOGVLSFWRGNLANVIRYPTQALNFAFKQKQIFLGVDKHTQFMRFPAGNLASGGA 157
 QY 124 GATSLCFVYPLDPAFTRILADVGKSGTEREERGLDCLVKTSDGIRGLYOGFSVVOG 183
 DB 158 GATSLCFVYPLDPAFTRILADVGKSGTEREERGLDCLVKTSDGIRGLYOGFSVVOG 216
 QY 184 IIVYRAVPEVVDPAKGL-PPKNTHTIVSMIAQTVTAAGVSPPTVRRMMQSG 242
 DB 217 IIVYRAVPEVVDPAKGL-PPKNTHTIVSMIAQTVTAAGVSPPTVRRMMQSG 276
 QY 243 GRKADIMYTGVDCKRKIFRDEGKAFKFGKAMSVNLKMGGAFLVLYDELKVI 298
 DB 277 --GGRQYNTIDCKKIIQNEGMSAMFKGALSNVFRGTGALVLAIDEIKFL 329

RESULT 15

S51132

ADP, ATP carrier protein - malaria parasite (Plasmodium falciparum)

N/Alternate names: ADP, ATP transporter

C/Species: Plasmodium falciparum

C/Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jun-2000

C/Accession: S51132

R/Hacin, I.; Jauregui, G.

Eur. J. Biochem. 228, 86-91, 1995

A/Title: Molecular characterization of the ADP/ATP-translocator cDNA from the human malar

A/Reference number: S51132; MUID:95188918; PMID:7883016

A/Accession: S51132

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-301 <HAT>

A/Cross-references: EMBL:X83551; NID:G623334; PIDN:CA58541.1; PID:G623335

C/Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

C/Keywords: duplication; transmembrane protein

F/6-102/Domain: ADP, ATP carrier protein repeat homology <ACPI>

F/112-203/Domain: ADP, ATP carrier protein repeat homology <ACR2>

F/209-301/Domain: ADP, ATP carrier protein repeat homology <ACR3>

Query Match 61.1%; Score 943; DB 2; Length 301;

Best Local Similarity 61.8%; Pred. No. 7.6e-76;

Matches 183; Conservative 45; Mismatches 62; Indels 6; Gaps 5;

7 SPADPLAGGIAAISTKTAAPIERVKLLQVGHASKQIAD--KQYGIYDCVIRIPK 64

```

Db      8 NPAADFLMGISAAISKVTPPIERVKMLIOTODSIPEIKSQOVERYSGLINCFKRVSK 67
Qy      65 OGVLSEFMRGNLANVIRYPTQALNFAPKDKYQIFLGVDKHTOPFWRYPAGNLASGGAAG 124
        68 OGVLSELMKGNVANVIRYPTQALNFAPKDYFNKIF-PRYDQNTDPSKFCVNLISGATAG 126
Qy      125 ATSLCFVYPLDPARTRLADVKGSGTEREFRLGDLVKITKSDGIRGLYOGFSYSVOGI 184
        127 AHSILIVYPLDPARTRLASDICK-GKDRQFTGLFDCLAKIYKQTLGLSLISGFGSVTGI 185
Qy      185 IIRAAIYGVTDYAKGML-PDPKXTHIVSWMIQOTVAAGVSYPPDTVRRMMMSG 243
        186 IYVRGSYFGLYDSAKALLFTNDKNTNIVLKNVAOSVTILAGLISYPPDTVRRMMMSG 245
Qy      244 RKG-ADIMYTGVDQWRKIFRDEGKAFPKGMSNVLRGMGAFTLVLYDELKXYI 298
        246 RKGKEIQKNTIDCMIKILNNEGFKFPKGAMANVIRGAGALVLYFYDELQKLI 301

```

Search completed: December 18, 2003, 12:44:05
 Job time : 15.3494 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2003, 12:37:01 ; Search time 30.701 Seconds

(without alignments)
2504.793 Million cell updates/sec

Title: US-09-811-131-33

Perfect score: 1543
Sequence: 1 MTEBQAI SPADFLAGIAIAA.....LRGNGAFVLVDELKKVI 298

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

SPTREMBL.23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_plage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriopl:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1474	95.5	298	13	Q8AYM3 O8AYM3 gallus galli
2	1451	94.0	298	6	Q8SOH5 Q8SOH5 bos taurus
3	1446	93.7	298	13	Q8JHI0 Q8JHI0 brachydanio
4	1422	92.2	298	6	O46373 O46373 oycoclaeas
5	1421	92.1	298	13	Q919M9 Q919M9 xenopus lae
6	1414	91.6	298	11	Q8BV19 Q8BV19 mus musculus
7	1409	91.3	298	13	Q9PRH1 Q9PRH1 rana rugosa
8	1406	91.1	298	13	Q9PRH2 Q9PRH2 rana rugosa
9	1402	90.9	298	13	Q9YIC4 Q9YIC4 rana rugosa
10	1300	84.3	299	5	Q8SVY4 Q8SVY4 ethomstigm
11	1259	81.6	317	13	Q91336 Q91336 rana sylvat
12	1254.5	81.3	312	5	Q8IRAO Q8IRAO drosophila
13	1235.5	80.1	300	5	Q9NHWS Q9NHWS lucilia cup
14	1187.5	77.0	288	5	O44093 O44093 drosophila
15	1183.5	76.7	288	5	O44094 O44094 drosophila
16	1176.5	76.2	304	5	Q25129 Q25129 halocynthia

17	1159	75.1	254	11	Q8BK05 Q8BK05 mus musculus
18	1137.5	73.7	307	5	O62526 O62526 drosophila
19	1119	72.5	315	4	Q9H0C2 Q9H0C2 homo sapien
20	1041	67.5	313	5	Q21103 Q21103 caenorhabdi
21	1039	67.3	313	5	P91410 P91410 caenorhabdi
22	1038	67.3	300	5	O45865 O45865 caenorhabdi
23	1036.5	67.2	310	10	O8H727 O8H727 phycophor
24	996	64.5	309	5	O97470 O97470 dictyosteli
25	993.5	64.4	300	5	O01813 O01813 caenorhabdi
26	993	64.4	300	5	O17407 O17407 caenorhabdi
27	973.5	63.1	318	5	Q9BJ36 Q9BJ36 toxoplasma
28	947	61.4	301	5	O81J34 O81J34 plasmodium
29	946.5	61.3	307	8	O9XM22 O9XM22 ascaris suu
30	944	61.2	301	5	O25692 O25692 plasmodium
31	944	61.2	301	5	Q8MYR4 Q8MYR4 eplotes sp
32	943	61.1	301	5	Q26006 Q26006 plasmodium
33	936	60.7	305	5	Q8MYR7 Q8MYR7 nyctotherus
34	932	60.4	308	5	Q8MYR8 Q8MYR8 nyctotherus
35	924	59.9	306	5	Q8MYR5 Q8MYR5 nyctotherus
36	924	59.9	308	5	Q8MYR6 Q8MYR6 nyctotherus
37	827	53.6	170	6	Q9X869 Q9X869 sus scrofa
38	778.5	50.5	305	3	Q9P8M1 Q9P8M1 yarrowia li
39	767.5	49.7	302	3	Q8J0M2 Q8J0M2 yarrowia li
40	764	49.5	326	5	P91270 P91270 caenorhabdi
41	760	49.3	307	5	O76286 O76286 trypsinosoma
42	759	49.2	303	3	O74260 O74260 candida par
43	756.5	49.0	306	5	Q18683 Q18683 caenorhabdi
44	753	48.8	307	5	Q26697 Q26697 trypsinosoma
45	749	48.5	315	3	O8J0U1 O8J0U1 gaeananomy

ALIGNMENTS

RESULT 1

ID Q8AYM3 PRELIMINARY; PRT; 298 AA.

AC Q8AYM3 (TREMBLREL.23, Created)

DT 01-MAR-2003 (TREMBLREL.23, Last sequence update)

DT 01-MAR-2003 (TREMBLREL.23, Last annotation update)

DE ATP/ADP antiporter.

GN AVANT.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archaeosuria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RA Toyomizu M., Ueda M., Sato S., Seki Y., Sato K., Akiba Y.,

RT "Cold-induced mitochondrial uncoupling and expression of chicken UCP

RL FEBS Lett. 0:0-0(2002).

DR EMBL, AB088686; BAC1553.1; -

SO SEQUENCE 298 AA; 32847 MW; 1174CC5BC400A10D CRC64;

Query Match 95.5%; Score 1474; DB 13; Length 298;

Best Local Similarity 93.0%; Pred. No. 2.5e-125;

Matches 277; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

QY 1 MTEBQAI SPADFLAGIAIAAISKTA VPIERVKLLLVQHASKOIADKQYKIVDCIVR 60

DB 1 MADQAI SFKDFLARGVAAAI SKTAVPIERVKLLLVQHASKOIADKQYKIVDCIVR 60

QY 61 IPKQGVLSFMRGNLAVIRYPTQALNFAFKDKYKQIPFGVVDKHOQFRRYFAGNLASG 120

DB 61 IPKQGVLSFMRGNLAVIRYPTQALNFAFKDKYKQIPFGVVDKHOQFRRYFAGNLASG 120

QY 121 GAAGATSLCFYPLDPARTLADVGRKSGTEREFGVGLDCLVKITKSGDGLVQGSFVS 180

DB 121 GAAGATSLCFYPLDPARTLADVGRKSGTEREFGVGLDCLVKITKSGDGLVQGSFVS 180

QY 181 VGGIIITRAAYFGVYDTRAKGMLPDPKNTHTIVSNMIAQTVAAGVSYPPDYRRMM 240
 DB 181 VGGIIITRAAYFGVYDTRAKGMLPDPKNTHTIVSNMIAQTVAAGVSYPPDYRRMM 240
 QY 241 QSGRKADIMTGTVDCKRKIFRDEGGKAFKAGMSNTLRGMAFVLYLDELKVI 298
 DB 241 QSGRKADIMTGTVDCKRKIFRDEGGKAFKAGMSNTLRGMAFVLYLDELKVI 298

RESULT 2

Q8SCH5 PRELIMINARY; PRT; 298 AA.

AC Q8SCH5
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Adenine nucleotide translocator 2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NC NCB1_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N. A.
 RA Yamazaki N., Shiohara Y., Tanida K., Terada H.;
 RT "Structural properties of mammalian mitochondrial ADP/ATP carriers:
 RT identification of possible amino acids that determine functional
 RT differences in its isoforms."
 RL Mitochondrion 1:371-379(2002).
 DR EMBL; AB065433; BAB84673.1;
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carrier.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 SQ SEQUENCE 298 AA; 32955 MW; CB6897BB987B79C0 CRC64;

Query Match 94.0%; Score 1451; DB 6; Length 298;

Best Local Similarity 92.2%; Pred. No. 3e-123; Matches 273; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTEPAISFADKPLAGGIAAISTKAVAPIERVKLLQVQHSKQITADKQKGIYDCTVR 60
 DB 1 MTEPAISFADKPLAGGIAAISTKAVAPIERVKLLQVQHSKQITADKQKGIYDCTVR 60
 QY 61 IPKQGVLSFWRGNLANVIRFPYTOALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLSG 120
 DB 61 IPKQGVLSFWRGNLANVIRFPYTOALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLSG 120
 QY 121 GAAGATSLCFYYPDLPARTRLAADVGKSGTEREFGDCLVKTGSDGIGLYQGFVS 180
 DB 121 GAAGATSLCFYYPDLPARTRLAADVGKSGTEREFGDCLVKTGSDGIGLYQGFVS 180
 QY 181 VGGIIITRAAYFGVYDTRAKGMLPDPKNTHTIVSNMIAQTVAAGVSYPPDYRRMM 240
 DB 181 VGGIIITRAAYFGVYDTRAKGMLPDPKNTHTIVSNMIAQTVAAGVSYPPDYRRMM 240
 QY 241 QSGRKADIMTGTVDCKRKIFRDEGGKAFKAGMSNTLRGMAFVLYLDELKVI 298
 DB 241 QSGRKADIMTGTVDCKRKIFRDEGGKAFKAGMSNTLRGMAFVLYLDELKVI 298

RESULT 3

Q8JH10 PRELIMINARY; PRT; 298 AA.

AC Q8JH10
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Solute carrier family 25 member 5 protein.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.

OX NCB1_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N. A.
 RX MEDLINE=22035902; PubMed=12006978;
 RA Gollig G., Amsterdam A., Sun Z., Antonelli M., Maldonado B., Chen W.,
 RA Burgess S., Hald M., Artzt K., Farrington S., Lin S.-Y., Nissen R.M.,
 RA Hopkins N.;
 RT "Insertional mutagenesis in zebrafish rapidly identifies genes
 RT essential for early vertebrate development."
 RL Nat. Genet. 31:135-140(2002).
 DR EMBL; AF506216; AAM34660.1;
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR Pfam; PF00153; mito_carrier.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 SQ SEQUENCE 298 AA; 32763 MW; D78663CF55C51D39 CRC64;

Query Match 93.7%; Score 1446; DB 13; Length 298;

Best Local Similarity 91.9%; Pred. No. 8.5e-123; Matches 274; Conservative 15; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEPAISFADKPLAGGIAAISTKAVAPIERVKLLQVQHSKQITADKQKGIYDCTVR 60
 DB 1 MTEPAISFADKPLAGGIAAISTKAVAPIERVKLLQVQHSKQITADKQKGIYDCTVR 60
 QY 61 IPKQGVLSFWRGNLANVIRFPYTOALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLSG 120
 DB 61 IPKQGVLSFWRGNLANVIRFPYTOALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLSG 120
 QY 121 GAAGATSLCFYYPDLPARTRLAADVGKSGTEREFGDCLVKTGSDGIGLYQGFVS 180
 DB 121 GAAGATSLCFYYPDLPARTRLAADVGKSGTEREFGDCLVKTGSDGIGLYQGFVS 180
 QY 181 VGGIIITRAAYFGVYDTRAKGMLPDPKNTHTIVSNMIAQTVAAGVSYPPDYRRMM 240
 DB 181 VGGIIITRAAYFGVYDTRAKGMLPDPKNTHTIVSNMIAQTVAAGVSYPPDYRRMM 240
 QY 241 QSGRKADIMTGTVDCKRKIFRDEGGKAFKAGMSNTLRGMAFVLYLDELKVI 298
 DB 241 QSGRKADIMTGTVDCKRKIFRDEGGKAFKAGMSNTLRGMAFVLYLDELKVI 298

RESULT 4

Q46373 PRELIMINARY; PRT; 298 AA.

AC Q46373
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE ADP/ATP translocase.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 NC NCB1_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC TISSUE=Skeletal muscle;
 RA Yamaguchi N., Kasai M.;
 RT "Identification of a 30kDa calsequestrin-binding protein, which
 RT regulates calcium release from sarcoplasmic reticulum of rabbit
 RT skeletal muscle."
 RL J. Biochem. 335:541-547(1998).
 DR EMBL; AB009386; BAA23777.1;
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR Pfam; PF00153; mito_carrier.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.

DR PROSITE; PS00215; MITOCH CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 32901 MW; CAA832C088164AD78 CRC64;

Query Match 92.2%; Score 1422; DB 6; Length 298;
Best Local Similarity 88.9%; Pred. No. 1.3e-120;
Matches 265; Conservative 20; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEQASIFAKDPLAGGIAAISTAVAPIERVKLLQVQHASKOIAADKOYGVDCIVR 60
DB 1 MSDQSLSTKDPFLAGGIAAASKTAVAPIERVKLLQVQHASKOISAKQYGIIDCVRR 60
QY 1PKEGVLSFMRGNLANVIRYPTQALNFAFKDKTKQIFLGVDKHTQFWRYFAGNLASG 120
DB 61 IPKGGFISFMRGNLANVIRYPTQALNFAFKDKTKQIFLGVDKHTQFWRYFAGNLASG 120
QY 121 GAAGATSLCFYVPLDPARTRLAADVGKSGTEREPRGLDCLVTKTSGINGLYOGFSVS 180
DB 121 GAAGATSLCFYVPLDPARTRLAADVGKGAAGREFSGLGNCLTKIKPSDGLRGLYOGFSVS 180
QY 181 VGGIITRYAAAFGVYDTRAKGMLPDPKNTHTIVSNMIAQTVAVAGVSPPTVRRRMM 240
DB 181 VGGIITRYAAAFGVYDTRAKGMLPDPKNTHTIVSNMIAQTVAVAGVSPPTVRRRMM 240
QY 241 QSGRKGADIMYTGVDCKRKLFRDEGKAFKFGKAMSNVLRGMAFVLVYDELKVI 298
DB 241 QSGRKGADIMYTGVDCKRKLAKDEGAKAFKFGKAMSNVLRGMAFVLVYDELKVI 298

RESULT 5

Q919M9 PRELIMINARY; PRT; 298 AA.
AC Q919M9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Adenine nucleotide translocase.
GN ANTL.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_Taxid=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Crawford M.J., Kiosrowskian F., Varmura S.L., Liverage R.A.;
RT "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific and
RT Dynamic Patterns of Expression During Development."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DB EMBL; AF213147; AAF63471.1; -
DB InterPro; IPR001993; Mitoch_carrier.
DB InterPro; IPR002067; Mlt_carrier.
DB InterPro; IPR002030; Mlt_uncoupling.
DB Pfam; PF00153; mito_carr; 3.
DB PRINTS; PR00926; MITOCARRIER.
DB PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 32940 MW; 91B740133751877F CRC64;

Query Match 92.1%; Score 1421; DB 13; Length 298;
Best Local Similarity 90.3%; Pred. No. 1.6e-120;
Matches 269; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEQASIFAKDPLAGGIAAISTAVAPIERVKLLQVQHASKOIAADKOYGVDCIVR 60
DB 1 MTEQASIFAKDPLAGGIAAISTAVAPIERVKLLQVQHASKOITADKHTKGIIDCVRR 60
QY 61 IPKGGVLSFMRGNLANVIRYPTQALNFAFKDKTKQIFLGVDKHTQFWRYFAGNLASG 120
DB 61 IPKGGVLSFMRGNLANVIRYPTQALNFAFKDKTKQIFLGVDKHTQFWRYFAGNLASG 120

QY 121 GAAGATSLCFYVPLDPARTRLAADVGKSGTEREPRGLDCLVTKTSGINGLYOGFSVS 180
DB 121 GAAGATSLCFYVPLDPARTRLAADVGKAMRERPRGLDCLVTKISKSGIKGLYOGFSVS 180
QY 181 VGGIITRYAAAFGVYDTRAKGMLPDPKNTHTIVSNMIAQTVAVAGVSPPTVRRRMM 240
DB 181 VGGIITRYAAAFGVYDTRAKGMLPDPKNTHTIVSNMIAQTVAVAGVSPPTVRRRMM 240

QY 241 QSGRKGADIMYTGVDCKRKLFRDEGKAFKFGKAMSNVLRGMAFVLVYDELKVI 298
DB 241 QSGRKGADIMYTGVDCKRKLARDGSKAFKFGKAMSNVLRGMAFVLVYDELKVI 298

RESULT 6

Q98BV9 PRELIMINARY; PRT; 298 AA.
AC Q98BV9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Solute carrier family 25.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA "The Riken Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK078077; BAC37117.1; -
SQ SEQUENCE 298 AA; 32904 MW; F94C8909836710B CRC64;

Query Match 91.6%; Score 1414; DB 11; Length 298;
Best Local Similarity 88.6%; Pred. No. 6.8e-120;
Matches 264; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTEQASIFAKDPLAGGIAAISTAVAPIERVKLLQVQHASKOIAADKOYGVDCIVR 60
DB 1 MGRKLSFLKDPFLAGGIAAASKTAVAPIERVKLLQVQHASKOISAKQYGIIDCVRR 60
QY 61 IPKGGVLSFMRGNLANVIRYPTQALNFAFKDKTKQIFLGVDKHTQFWRYFAGNLASG 120
DB 61 IPKGGFISFMRGNLANVIRYPTQALNFAFKDKTKQIFLGVDKHTQFWRYFAGNLASG 120
QY 121 GAAGATSLCFYVPLDPARTRLAADVGKSGTEREPRGLDCLVTKTSGINGLYOGFSVS 180
DB 121 GAAGATSLCFYVPLDPARTRLAADVGKSGTEREPRGLDCLVTKTSGINGLYOGFSVS 180
QY 181 VGGIITRYAAAFGVYDTRAKGMLPDPKNTHTIVSNMIAQTVAVAGVSPPTVRRRMM 240
DB 181 VGGIITRYAAAFGVYDTRAKGMLPDPKNTHTIVSNMIAQTVAVAGVSPPTVRRRMM 240
QY 241 QSGRKGADIMYTGVDCKRKLFRDEGKAFKFGKAMSNVLRGMAFVLVYDELKVI 298
DB 241 QSGRKGADIMYTGVDCKRKLAKDEGAKAFKFGKAMSNVLRGMAFVLVYDELKVI 298

RESULT 7

Q9PRH1 PRELIMINARY; PRT; 298 AA.
AC Q9PRH1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (Wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.

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CX NCB1_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99083429; PubMed=9866197;
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB008463; BAA36513.1; -
DR EMBL; AB008456; BAA36506.1; -
DR EMBL; AB008461; BAA36511.1; -
DR EMBL; AB008462; BAA36512.1; -
DR InterPro; IPR001993; Mitoch carrier.
DR InterPro; IPR002067; Mlt carrier.
DR InterPro; IPR002030; Mlt uncoupling.
DR Pfam; PF00153; mito_carr_3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00784; MTNCOUPLING.
DR PROSITE; PS00215; MITOCH CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33054 MW; B0E23AD56F548D36 CRC64;

Query Match 91.3%; Score 1409; DB 13; Length 298;
Best Local Similarity 88.6%; Pred. No. 1.9e-119;
Matches 264; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEOASFAKDFLAGGIAAISKTAIVAPIERVKLLQVQHASKOJADKOYGYVDCIVR 60
DB 1 MTDALISFAKDFLAGGVAIAISKTAIVAPIERVKLLQVQHASKOJADKOYGYVDCIVR 60
QY 61 IPKGGVLSFWKGNLANIRYFPQTALNFAFKDKTKYKIFLGVDKHTQFWRYFAGNLSG 120
DB 61 IPKGGVLSFWKGNLANIRYFPQTALNFAFKDKTKYKIFLGVDKHTQFWRYFAGNLSG 120
QY 121 GAAGATSLCFYYPDPFATRLAADVGKSGTEREFGGLDCLVKTISDGIKGLYGFSEVS 180
DB 121 GAAGATSLCFYYPDPFATRLAADVGKSGTEREFGGLDCLVKTISDGIKGLYGFSEVS 180
QY 181 VGGIIYRAAYFGVYDTAKGMLPDPKNTHTIVSWMIAGTVAVAGVSYPPDTVRRMM 240
DB 181 VGGIIYRAAYFGVYDTAKGMLPDPKNTHTIFSMIAQTVAVAGFASYPDTVRRMM 240
QY 241 QSGRKGADIMTYGVDCWKRIFRDEGGAFFKGAWSNVLKMGAFVLYLDELKVI 298
DB 241 QSGRKGADIMTYGVDCWKRIARDEGSAFFKGAWSNVLKMGAFVLYLDELKVI 298

RESULT 8
QYPRH2 PRELIMINARY; PRT; 298 AA.
AC QYPRH2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DB ADP/ATP translocase.
OS Rana rugosa (wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
CX NCB1_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99083429; PubMed=9866197;
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB008460; BAA36510.1; -
DR EMBL; AB008458; BAA36508.1; -
DR EMBL; AB008459; BAA36509.1; -

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DR InterPro; IPR001993; Mitoch carrier.
DR InterPro; IPR002067; Mlt carrier.
DR InterPro; IPR002030; Mlt uncoupling.
DR Pfam; PF00153; mito_carr_3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTNCOUPLING.
DR PROSITE; PS00215; MITOCH CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33082 MW; B0E225E867599A06 CRC64;

Query Match 91.1%; Score 1406; DB 13; Length 298;
Best Local Similarity 88.3%; Pred. No. 3.6e-119;
Matches 263; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEOASFAKDFLAGGIAAISKTAIVAPIERVKLLQVQHASKOJADKOYGYVDCIVR 60
DB 1 MTDALISFAKDFLAGGVAIAISKTAIVAPIERVKLLQVQHASKOJADKOYGYVDCIVR 60
QY 61 IPKGGVLSFWKGNLANIRYFPQTALNFAFKDKTKYKIFLGVDKHTQFWRYFAGNLSG 120
DB 61 IPKGGVLSFWKGNLANIRYFPQTALNFAFKDKTKYKIFLGVDKHTQFWRYFAGNLSG 120
QY 121 GAAGATSLCFYYPDPFATRLAADVGKSGTEREFGGLDCLVKTISDGIKGLYGFSEVS 180
DB 121 GAAGATSLCFYYPDPFATRLAADVGKSGTEREFGGLDCLVKTISDGIKGLYGFSEVS 180
QY 181 VGGIIYRAAYFGVYDTAKGMLPDPKNTHTIVSWMIAGTVAVAGVSYPPDTVRRMM 240
DB 181 VGGIIYRAAYFGVYDTAKGMLPDPKNTHTIFSMIAQTVAVAGFASYPDTVRRMM 240
QY 241 QSGRKGADIMTYGVDCWKRIFRDEGGAFFKGAWSNVLKMGAFVLYLDELKVI 298
DB 241 QSGRKGADIMTYGVDCWKRIARDEGSAFFKGAWSNVLKMGAFVLYLDELKVI 298

RESULT 9
QYITC4 PRELIMINARY; PRT; 298 AA.
AC QYITC4;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DB ADP/ATP translocase.
OS Rana rugosa (wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
CX NCB1_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99083429; PubMed=9866197;
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB008457; BAA36507.1; -
DR InterPro; IPR001993; Mitoch carrier.
DR InterPro; IPR002067; Mlt carrier.
DR InterPro; IPR002030; Mlt uncoupling.
DR Pfam; PF00153; mito_carr_3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTNCOUPLING.
DR PROSITE; PS00215; MITOCH CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 15B270ED37099A00 CRC64;

Query Match 90.9%; Score 1402; DB 13; Length 298;
Best Local Similarity 87.9%; Pred. No. 8.3e-119;
Matches 262; Conservative 21; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEOASFAKDFLAGGIAAISKTAIVAPIERVKLLQVQHASKOJADKOYGYVDCIVR 60
DB 1 MTDALISFAKDFLAGGVAIAISKTAIVAPIERVKLLQVQHASKOJADKOYGYVDCIVR 60

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Db 1 MTDAAISPAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKOITADKQYKIMDCVVR 60
 QY 1PKEQGVLSFMRGNLANVIRFFPTQALNFAFKDKTKOIFLGVDKHTQFMRYFAGNLASG 120
 Db 61 IPKEQGVLSFMRGNLANVIRFFPTQALNFAFKDKTKOIFLNDVDRKTPFMRYPAGNLASG 120
 QY 121 GAAGATSLCFYVPLDPARTRLAADVGKSGTEREFGGLDCLVTKYSDGIRGLYQGFVS 180
 Db 121 GAAGATSLCFYVPLDPARTRLAADVGKSGTEREFGGLDCLVTKYSDGIRGLYQGFVS 180
 QY 181 VOGIIITRAAFVGYDTRAKGMLPDPKNTHTIVSMIAQVTAAGVSVYPDTRRRMM 240
 Db 181 VOGIIITRAAFVGYDTRAKGMLPDPKNTHTIVSMIAQVTAAGVSVYPDTRRRMM 240
 QY 241 OSGRKADIMYTGVDKCRKIFRDEGKAFKFGKANSVLRGKGFVVLVDLKKVI 298
 Db 241 OSGRKADIMYTGVDKCRKIFRDEGKAFKFGKANSVLRGKGFVVLVDLKKVI 298

RESULT 10

Q95VX4 PRELIMINARY; PRT; 299 AA.
 AC Q95VX4
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE ADP-ATP translocase.
 OS Ethmostigmus rubripes.
 OC Eukaryota; Metazoa; Arthropoda; Myriapoda; Chilopoda;
 OC Pleurostigmophora; Scolopendromorpha; Scolopendridae; Ethmostigmus.
 OX NCBI_TaxId=62613;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Burnell J.N.;
 RT "Nucleotide sequence of an ADP-ATP translocator of Ethmostigmus
 rubripes";
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 RL EMBL; AF401758; AAL02100.1; -;
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mlt_carrier.
 DR Pfam; PF00153; mltc_carrier; 3.
 DR PRINTS; PR00926; MITOCARIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 SQ SEQUENCE 299 AA; 33037 MW; 3C3BCB26E7C3C5E CRC64;

Query Match 84.3%; Score 1300; DB 5; Length 299;
 Best Local Similarity 81.5%; Pred. No. 1.5e-109;
 Matches 243; Conservative 26; Mismatches 29; Indels 0; Gaps 0;

QY 1 MTDAAISPAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKOITADKQYKIMDCVVR 60
 Db 1 MTDAAISPAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKOITADKQYKIMDCVVR 60
 QY 61 IPKEQGVLSFMRGNLANVIRFFPTQALNFAFKDKTKOIFLGVDKHTQFMRYFAGNLASG 120
 Db 61 IPKEQGVLSFMRGNLANVIRFFPTQALNFAFKDKTKOIFLNDVDRKTPFMRYPAGNLASG 120
 QY 121 GAAGATSLCFYVPLDPARTRLAADVGKSGTEREFGGLDCLVTKYSDGIRGLYQGFVS 180
 Db 121 GAAGATSLCFYVPLDPARTRLAADVGKSGTEREFGGLDCLVTKYSDGIRGLYQGFVS 180
 QY 181 VOGIIITRAAFVGYDTRAKGMLPDPKNTHTIVSMIAQVTAAGVSVYPDTRRRMM 240
 Db 181 VOGIIITRAAFVGYDTRAKGMLPDPKNTHTIVSMIAQVTAAGVSVYPDTRRRMM 240
 QY 241 OSGRKADIMYTGVDKCRKIFRDEGKAFKFGKANSVLRGKGFVVLVDLKKVI 298
 Db 241 OSGRKADIMYTGVDKCRKIFRDEGKAFKFGKANSVLRGKGFVVLVDLKKVI 298

RESULT 11
 Q91336 PRELIMINARY; PRT; 317 AA.

AC Q91336;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE ADP/ATP translocase.
 OS Rana sylvatica (Wood frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
 OX NCBI_TaxId=45438;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=Liver;
 RC MEDLINE=97398141; PubMed=9256066;
 RA Cai Q., Greenway S.C., Storey K.B.;
 RT "Differential regulation of the mitochondrial ADP/ATP translocase gene
 in wood frog under freezing stress";
 RL Biochim. Biophys. Acta 1353:69-78 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Cai Q., Storey K.B.;
 RL Submitted (APR-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; U44832; AAA97882.2; -;
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mlt_carrier.
 DR Pfam; PF00153; mltc_carrier; 3.
 DR PRINTS; PR00926; MITOCARIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Membrane; Transmembrane; Transport.
 SQ SEQUENCE 317 AA; 35005 MW; 5F66B7BD8D5CEB72 CRC64;

Query Match 81.6%; Score 1259; DB 13; Length 317;
 Best Local Similarity 86.8%; Pred. No. 8.2e-106;
 Matches 236; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

QY 1 MTDAAISPAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKOITADKQYKIMDCVVR 60
 Db 1 MTDAAISPAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKOITADKQYKIMDCVVR 60
 QY 61 IPKEQGVLSFMRGNLANVIRFFPTQALNFAFKDKTKOIFLGVDKHTQFMRYFAGNLASG 120
 Db 61 IPKEQGVLSFMRGNLANVIRFFPTQALNFAFKDKTKOIFLNDVDRKTPFMRYPAGNLASG 120
 QY 121 GAAGATSLCFYVPLDPARTRLAADVGKSGTEREFGGLDCLVTKYSDGIRGLYQGFVS 180
 Db 121 GAAGATSLCFYVPLDPARTRLAADVGKSGTEREFGGLDCLVTKYSDGIRGLYQGFVS 180
 QY 181 VOGIIITRAAFVGYDTRAKGMLPDPKNTHTIVSMIAQVTAAGVSVYPDTRRRMM 240
 Db 181 VOGIIITRAAFVGYDTRAKGMLPDPKNTHTIVSMIAQVTAAGVSVYPDTRRRMM 240
 QY 241 OSGRKADIMYTGVDKCRKIFRDEGKAFK 272
 Db 241 OSGRKADIMYTGVDKCRKIFRDEGKAFK 272

RESULT 12
 Q81RAO PRELIMINARY; PRT; 312 AA.
 AC Q81RAO
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE CG16944-PC.
 GN SE8.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxId=7227;
 RN [1]
 RP SEQUENCE FROM N.A.

RA MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celinkner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abail J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benson P.V., Bertone P., Bhandari D., Bolshakov S.,
 RA Borkov D., Borcher M.R., Bouck J., Brokstein P., Brotter P.,
 RA Butris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo J.B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
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 RA SEQUENCE FROM N.A.
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 RA "Sequencing of *Drosophila melanogaster* genome.";
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 RA "Annotation of *Drosophila melanogaster* genome.";
 RA Submitted (Mar-2000) to the EMBL/Genbank/DBJ databases.
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 RA SEQUENCE FROM N.A.
 RA Adams M.D., Celinkner S.E., Gibbs R.A., Rubin G.M., Venter J.C.;
 RA Submitted (Mar-2000) to the EMBL/Genbank/DBJ databases.
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 RA SEQUENCE FROM N.A.

RA FlyBase;
 RA Submitted (SEP-2002) to the EMBL/Genbank/DBJ databases.
 RA EMBL; AB003484; AAN09267.1;
 RA SEQUENCE 312 AA; 34214 MW; 78D5834E74E168DF CRC64;
 RA Query Match 81.3%; Score 1254.5; DB 5; Length 312;
 RA Best Local Similarity 80.6%; Pred. No. 2.1e-105;
 RA Matches 237; Conservative 23; Mismatches 33; Indels 1; Gaps 1;
 QY 5 AIFAKDPLAGIAAIAISKTVAPIERVKLLQVQHASKOIAADKQKGIYDCIARIPE 64
 DB 20 AVGFYKDPAGGISAASVKTAVAPIERVKLLQVQHSIKQISPDQKGMVDCFIARIPE 79
 QY 65 QGVLSFWNGNLANVIRYPTQALNFAFKQKQIFLGVDKHTQWRYPAGNLASGGAAG 124
 DB 80 QGFSSFWNGNLANVIRYPTQALNFAFKQKQIFLGVDKHTQWRYPAGNLASGGAAG 139
 QY 125 ATSLCFVYPLDPARTRLAADVGSGTREPGLGCLVKTKRSDIRGLYQGSFVSVOGI 184
 DB 140 ATSLCFVYPLDPARTRLAADVGSG-ONEFTGLGCLVKTKRSDIYGLYQGSFVSVOGI 198
 QY 185 IYRAAYFGVYDTAKGMLPDPKNTIIVSWIAQTVAAGVSYFPDTRRRMMQSGR 244
 DB 199 IYRAAYFGVYDTAKGMLPDPKNTIIVSWIAQVTVVAGVSYFPDTRRRMMQSGR 258
 QY 245 KGADIMYGTVDQWKRIFRDEGKAPFFGAMSNTVRGKGAFAVLYYBELKVI 298
 DB 259 KATEVIYKNTLHCWATIKAGGTGAFFGAFSNIIRGTGAFVLYYBELKVI 312
 RESULT 13
 ID Q9NHM5 PRELIMINARY; PRT; 300 AA.
 AC Q9NHM5;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DB ADP/ATP translocase.
 OS *Lucilia cuprina* (Greenbottle fly) (Australian sheep blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; *Lucilia*.
 OK NCBI_Taxid=7375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SS mal seeking;
 RA Chen Z., Pair J.A., Batterham P.;
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC EMBL; AF218587; AAF32322.1;
 DR InterPro: IPR001993; Mitoch carrier.
 DR InterPro: IPR002067; Mit carrier.
 DR Pfam: PF00153; mito carri 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER, 3.
 KW Membrane; Transmembrane; Transport.
 SQ SEQUENCE 300 AA; 33036 MW; 5459D0EAD0E28742 CRC64;
 QY Query Match 80.1%; Score 1235.5; DB 5; Length 300;
 QY Best Local Similarity 79.5%; Pred. No. 1e-103;
 QY Matches 233; Conservative 24; Mismatches 35; Indels 1; Gaps 1;
 DB 9 LGFVDFPAAGGISAASVKTAVAPIERVKLLQVQHSIKQISPDQKGMVDCFIARIPE 68
 QY 66 GVLTSFWNGNLANVIRYPTQALNFAFKQKQIFLGVDKHTQWRYPAGNLASGGAAG 125
 DB 69 GFASTYRWGNNANVIRYPTQALNFAFKQKQIFLGVDKHTQWRYPAGNLASGGAAG 128
 QY 126 TSLCFVYPLDPARTRLAADVGSGTREPGLGCLVKTKRSDIRGLYQGSFVSVOGI 185

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Db 129 TSLCFVYPLDFAFRTLAADTGKG-QREFTGLGNCILAKIPKSGDVGLYRGFGVSGI 187
QY 166 IYRAAYFGVYDPAKGMPLDPKNTIIVSMIAQTAVAGVSYPPDTRRRMMQSGR 245
Db 188 IYRAAYFGVYDPAKGMPLDPKNTIIVSMIAQTAVAGVSYPPDTRRRMMQSGR 247
QY 246 GADIMYGTVDGCKRIFRDEGKAFPGKANSVLRGNGAFVLY 289
Db 248 ATETIYKNTLHCWATIAKQEGTGAFFKAFSNVLRGTGAFVLYDELKEL 300

RESULT 14
044093 PRELIMINARY; PRT; 288 AA.
AC 044093:
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE ADP/ATP translocase (Fragment).
GN SSB.
OS Drosophila pseudobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxId=7237;
RN [1]
RP SEQUENCE FROM N.A.
RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.,
CC Genetics 0:0-0(1997).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AF025799; AAB87883.1; -.
DR FLYbase; FBgn0023237; Dros\seeb.
DR InterPro; IPR001993; Mitoch\_carrier.
DR InterPro; IPR002067; Mito\_carrier.
DR Pfam; PF00153; mito\_carf; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH CARRIER; 3.
KW Membrane; Repeat; Transmembrane; Transport.
FT NON TER 288
SQ SEQUENCE 288 AA; 31725 MW; 052B0CC050436B0 CRC64;

Query Match 77.0%; Score 1187.5; DB 5; Length 288;
Best Local Similarity 80.7%; Pred. No. 2.2e-99;
Matches 230; Conservative 19; Mismatches 33; Indels 3; Gaps 3;

QY 5 AISPADFLAGGIAAISKTAVAPIERVKLLQVGHASKQIADQYKGIYDCIVRIPE 64
Db 7 AIGFYKDFPAAAGISAASVKTAVAPIERVKLLQVGHISKQISPDQYKGMVDCFIRIPE 66
QY 65 QGVLSFMRGNLANVIRYPTQALNPAFDKTKQIFLGVDKHTQWRPFAAGTLASGGAAG 124
Db 67 QGFSSFWRGNLANVIRYPTQALNPAFDKTKQIFLGVDKHTQWRPFAAGTLASGGAAG 126
QY 125 ATSLCFVYPLDFAFRTLAADVGKSGTEREFGDCLVITKSDGIRGLYOGFSVSGI 184
Db 127 ATSLCFVYPLDFAFRTLAADVGKSG-QREFTGLGNCILAKIPKSGDVGLYRGFGVSGI 185
QY 185 IYRAAYFGVYDPAKGMPLDPKNTIIVSMIAQTAVAGVSYPPDTRRRMMQSGR 244
Db 186 IYRAAYFGVYDPAKGMPLDPKNTIIVSMIAQTAVAGVSYPPDTRRRMMQSGR 244
QY 245 KADIMYGTVDGCKRIFRDEGKAFPGKANSVLRGNGAFVLY 289
Db 248 KATETIYKNTLHCWATIAKQEGTGAFFKAFSNVLRGTGAFVLY 288

RESULT 15
044094 PRELIMINARY; PRT; 288 AA.
AC 044094:
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

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DE ADP/ATP translocase (Fragment).
GN SSB.
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxId=7241;
RN [1]
RP SEQUENCE FROM N.A.
RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.,
CC Genetics 0:0-0(1997).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AF025799; AAB87884.1; -.
DR FLYbase; FBgn0023237; Dros\seeb.
DR InterPro; IPR001993; Mitoch\_carrier.
DR InterPro; IPR002067; Mito\_carrier.
DR Pfam; PF00153; mito\_carf; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH CARRIER; 3.
KW Membrane; Repeat; Transmembrane; Transport.
FT NON TER 288
SQ SEQUENCE 288 AA; 31775 MW; 06A1D1E477B81B26 CRC64;

Query Match 76.7%; Score 1183.5; DB 5; Length 288;
Best Local Similarity 80.4%; Pred. No. 5e-99;
Matches 229; Conservative 20; Mismatches 33; Indels 3; Gaps 3;

QY 5 AISPADFLAGGIAAISKTAVAPIERVKLLQVGHASKQIADQYKGIYDCIVRIPE 64
Db 7 AMGFYKDFPAAAGISAASVKTAVAPIERVKLLQVGHISKQISPDQYKGMVDCFIRIPE 66
QY 65 QGVLSFMRGNLANVIRYPTQALNPAFDKTKQIFLGVDKHTQWRPFAAGTLASGGAAG 124
Db 67 QGFSSFWRGNLANVIRYPTQALNPAFDKTKQIFLGVDKHTQWRPFAAGTLASGGAAG 126
QY 125 ATSLCFVYPLDFAFRTLAADVGKSGTEREFGDCLVITKSDGIRGLYOGFSVSGI 184
Db 127 ATSLCFVYPLDFAFRTLAADVGKSG-QREFTGLGNCILAKIPKSGDVGLYRGFGVSGI 185
QY 185 IYRAAYFGVYDPAKGMPLDPKNTIIVSMIAQTAVAGVSYPPDTRRRMMQSGR 244
Db 186 IYRAAYFGVYDPAKGMPLDPKNTIIVSMIAQTAVAGVSYPPDTRRRMMQSGR 244
QY 245 KADIMYGTVDGCKRIFRDEGKAFPGKANSVLRGNGAFVLY 289
Db 248 KATETIYKNTLHCWATIAKQEGTGAFFKAFSNVLRGTGAFVLY 288

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